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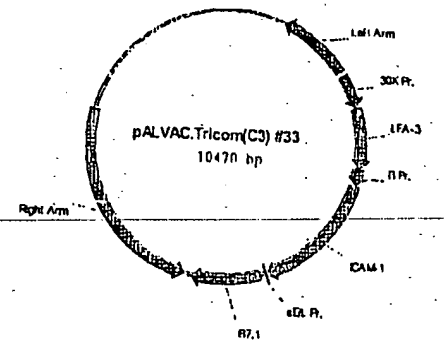
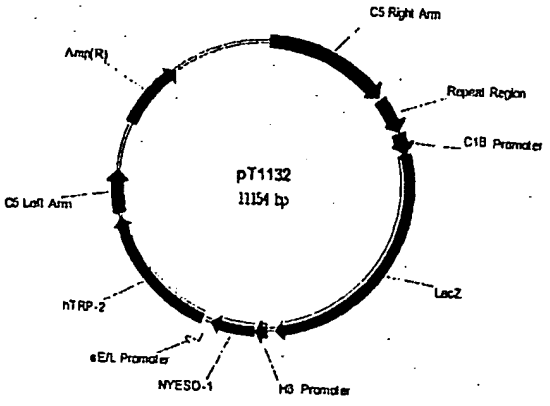
(54) Title: MULTI-ANTIGEN VECTORS FOR MELANOMA





(57) Abstract: The present invention relates to peptides, polypeptides, and nucleic acids and the use of the peptide, polypeptide or nucleic acid in preventing and / or treating cancer. In particular, the invention relates to peptides and nucleic acid sequences encoding such peptides for use in diagnosing, treating, or preventing melanoma.

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Multi-Antigen Vectors for Melanoma

FIELD OF THE INVENTION

The present invention relates to multi-antigen vectors for use in preventing and / or treating cancer. In particular, the invention relates to multi-antigen vectors for use in treating and/or preventing melanoma.

BACKGROUND OF THE INVENTION

There has been tremendous increase in last few years in the development of cancer vaccines with tumour-associated antigens (TAAs) due to the great advances in identification of molecules based on the expression profiling on primary tumours and normal cells with the help of several techniques such as high density microarray, SEREX, immunohistochemistry (IHC), RT-PCR, in-situ hybridization (ISH) and laser capture microscopy (Rosenberg, Immunity, 1999; Sgroi et al, 1999, Schena et al, 1995, Offringa et al, 2000). The TAAs are antigens expressed or over-expressed by tumour cells and could be specific to one or several tumours for example CEA antigen is expressed in colorectal, breast and lung cancers. Sgroi et al (1999) identified several genes differentially expressed in invasive and metastatic carcinoma cells with combined use of laser capture microdissection and cDNA microarrays. Several delivery systems like DNA or viruses could be used for therapeutic vaccination against human cancers (Bonnet et al, 2000) and can elicit immune responses and also break immune tolerance against TAAs. Tumour cells can be rendered more immunogenic by inserting transgenes encoding T cell co-stimulatory molecules such as B7.1 or cytokines such as IFN-γ, IL2, or GM-CSF, among others. Co-expression of a TAA and a cytokine or a co-stimulatory molecule can develop effective therapeutic vaccine (Hodge et al, 95, Bronte et al, 1995, Chamberlain et al, 1996).

There is a need in the art for reagents and methodologies useful in stimulating an immune response to prevent or treat cancers. The present invention provides such reagents and methodologies that overcome many of the difficulties encountered by others in attempting to treat cancer.

SUMMARY OF THE INVENTION

The present invention provides multi-antigen vectors for administration to a patient to prevent and / or treat cancer. In particular, the multi-antigen vector encodes one or more tumor antigens ("TA"). The multi-antigen vector may also encode an immune stimulator such as a co-stimulatory molecule and/or be administered with an adjuvant.

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1. Schematic of plasmids pALVAC.Tricom(#33) and pT1132.

Figure 2. DNA sequence of plasmid pALVAC.Tricom(#33).

Figure 3. DNA sequence of plasmid pT1132.

Figure 4. Schematic of plasmid pT3217.

Figure 5. DNA sequence of plasmid pT3217.

Figure 6. Amino acid sequences of exemplary NY-ESO-1, TRP-2, gp100, gp100M, MART-1, MAGE-1, MAGE-3, B7.1, LFA-3, and ICAM-1 proteins.

DETAILED DESCRIPTION

The present invention provides reagents and methodologies useful for treating and / or preventing cancer. All references cited within this application are incorporated by reference.

In one embodiment, the present invention relates to the induction or enhancement of an immune response against one or more tumor antigens ("TA") to prevent and / or treat cancer. In certain embodiments, one or more TAs may be combined. In preferred embodiments, the immune response results from expression of a TA in a host cell following administration of a nucleic acid vector encoding the tumor antigen or the tumor antigen itself in the form of a peptide or polypeptide, for example.

As used herein, an "antigen" is a molecule (such as a polypeptide) or a portion thereof that produces an immune response in a host to whom the antigen has been administered. The immune response may include the production of antibodies that bind to at least one epitope of the antigen and / or the generation of a cellular immune response against cells expressing an epitope of the antigen. The response may be an enhancement of a current immune response by, for example, causing increased antibody production, production of antibodies with increased affinity for the antigen, or an increase in the cellular immune response (i.e., increased number or activity

of immunoreactive T cells). An antigen that produces an immune response may alternatively be referred to as being immunogenic or as an immunogen. In describing the present invention, a TA may be referred to as an "immunogenic target". The present invention provide expression vectors for expressing in a host one or more immunogenic targets.

The term TA includes both tumor-associated antigens (TAAs) and tumor-specific antigens (TSAs), where a cancerous cell is the source of the antigen. A TAA is an antigen that is expressed on the surface of a tumor cell in higher amounts than is observed on normal cells or an antigen that is expressed on normal cells during fetal development. A TSA is an antigen that is unique to tumor cells and is not expressed on normal cells. TA further includes TAAs or TSAs, antigenic fragments thereof, and modified versions that retain their antigenicity.

TAs are typically classified into five categories according to their expression pattern, function, or genetic origin: cancer-testis (CT) antigens (i.e., MAGE, NY-ESO-1); melanocyte differentiation antigens (i.e., Melan A/MART-1, tyrosinase, gp100); mutational antigens (i.e., MUM-1, p53, CDK-4); overexpressed 'self' antigens (i.e., HER-2/neu, p53); and, viral antigens (i.e., HPV, EBV). For the purposes of practicing the present invention, a suitable TA is any TA that induces or enhances an anti-tumor immune response in a host to whom the TA has been administered. Suitable TAs include, for example, species of gp100 (Cox et al., *Science*, 264:716-719 (1994); U.S. Pat. No. 6,500,919 B1 and WO 01/30847 with Val at residue 162, also referred to as "gp100M"; U.S. Pat. No. 6,537,560 B1 with Phe at residue 162), MART-1/Melan A (Kawakami et al., *J. Exp. Med.*, 180:347-352 (1994); U.S. Pat. No. 5,874,560), gp75 (TRP-1) (Wang et al., *J. Exp. Med.*, 186:1131-1140 (1996)), TRP-2 (Wang et al. 1996 J. Exp. Med. 184:2207; U.S. Pat. Nos. 5,831,016 and 6,083,783), tyrosinase (Wolfel et al., *Eur. J. Immunol.*, 24:759-764 (1994); WO 200175117; WO 200175016; WO 200175007), NY-ESO-1 (WO 98/14464; WO 99/18206; GenBank Accession No. P78358; U.S. Pat. No. 5,804,381), melanoma proteoglycan (Hellstrom et al., *J. Immunol.*, 130:1467-1472 (1983)), MAGE family antigens (i.e., MAGE-1, 2,3,4,6,12, 51; Van der Bruggen et al., *Science*, 254:1643-1647 (1991); U.S. Pat. Nos. 6,235,525; CN 1319611), BAGE family antigens (Boel et al., *Immunity*, 2:167-175 (1995)), GAGE family antigens (i.e., GAGE-1,2; Van den Eynde et al., *J. Exp. Med.*, 182:689-698 (1995); U.S. Pat. No. 6,013,765), RAGE family antigens (i.e., RAGE-1; Gaugler et at., *Immunogenetics*, 44:323-330 (1996); U.S. Pat. No. 5,939,526), N-acetylglucosaminyltransferase-V (Guilloux et at., *J. Exp. Med.*, 183:1173-1183 (1996)), p15 (Robbins et al., *J. Immunol.*

154:5944-5950 (1995)), ß-catenin (Robbins et al., *J. Exp. Med.*, 183:1185-1192 (1996)); MUM-1 (Coulie et al., *Proc. Natl. Acad. Sci.* USA, 92:7976-7980 (1995)), cyclin dependent kinase-4 (CDK4) (Wolfel et al., *Science*, 269:1281-1284 (1995)), p21-*ras* (Fossum et at., *Int. J. Cancer*, 56:40-45 (1994)), BCR-*abl* (Bocchia et al., *Blood*, 85:2680-2684 (1995)), p53 (Theobald et al., *Proc. Natl. Acad. Sci.* USA, 92:11993-11997 (1995)), p185 HER2/neu (erb-B1; Fisk et al., *J. Exp. Med.*, 181:2109-2117 (1995)), epidermal growth factor receptor (EGFR) (Harris et al., Breast Cancer Res. Treat, 29:1-2 (1994)), carcinoembryonic antigens (CEA) (Kwong et al., *J. Natl. Cancer Inst.*, 85:982-990 (1995) U.S. Pat. Nos. 5,756,103; 5,274,087; 5,571,710; 6,071,716; 5,698,530; 6,045,802; EP 263933; EP 346710; and, EP 784483); carcinoma-associated mutated mucins (i.e., MUC-1 gene products; Jerome et al., *J. Immunol.*, 151:1654-1662 (1993)); EBNA gene products of EBV (i.e., EBNA-1; Rickinson et al., *Cancer Surveys*, 13:53-80 (1992)); E7, E6 proteins of human papillomavirus (Ressing et al., *J. Immunol*, 154:5934-5943 (1995)); prostate specific antigen (PSA; Xue et al., *The Prostate*, 30:73-78 (1997)); prostate specific membrane antigen (PSMA; Israeli, et al., *Cancer Res.*, 54:1807-1811 (1994)); idiotypic epitopes or antigens, for example, immunoglobulin idiotypes or T cell receptor idiotypes (Chen et al., *J. Immunol.*, 153:4775-4787 (1994)); KSA (U.S. Patent No. 5,348,887), kinesin 2 (Dietz, et al. Biochem Biophys Res Commun 2000 Sep 7;275(3):731-8), HIP-55, TGFβ-1 anti-apoptotic factor (Toomey, et al. Br J Biomed Sci 2001;58(3):177-83), tumor protein D52 (Bryne J.A., et al., Genomics, 35:523-532 (1996)), H1FT, NY-BR-1 (WO.01/47959), NY-BR-62, NY-BR-75, NY-BR-85, NY-BR-87, NY-BR-96 (Scanlan, M. Serologic and Bioinformatic Approaches to the Identification of Human Tumor Antigens, in *Cancer Vaccines 2000*, Cancer Research Institute, New York, NY), including "wild-type" (i.e., normally encoded by the genome, naturally-occurring), modified, and mutated versions as well as other fragments and derivatives thereof. Any of these TAs may be utilized alone or in combination with one another in a co-immunization protocol.

Preferred TAs are useful for inducing an immune response against melanoma cells. The term "melanoma" includes but is not limited to melanomas, metastatic melanomas, melanomas derived from either melanocytes or melanocyte related nevus cells, melanocarcinomas, melanoepitheliomas, melanosarcomas, melanoma *in situ*, superficial spreading melanoma, nodular melanoma, lentigo maligna melanoma, acral lentiginous melanoma, invasive melanoma and familial atypical mole and melanoma (FAM-M) syndrome, for example. In general,

melanomas result from chromosomal abnormalities, degenerative growth and development disorders, mitogenic agents, ultraviolet radiation (UV), viral infections, inappropriate tissue expression of a gene, alterations in expression of a gene or carcinogenic agents, for example.

In certain cases, it may be beneficial to co-immunize patients with both TA and other antigens, such as angiogenesis-associated antigens ("AA"). An AA is an immunogenic molecule (i.e., peptide, polypeptide) associated with cells involved in the induction and / or continued development of blood vessels. For example, an AA may be expressed on an endothelial cell ("EC"), which is a primary structural component of blood vessels. Where the cancer is cancer, it is preferred that that the AA be found within or near blood vessels that supply a tumor. Immunization of a patient against an AA preferably results in an anti-AA immune response whereby angiogenic processes that occur near or within tumors are prevented and / or inhibited. Exemplary AAs include, for example, vascular endothelial growth factor (i.e., VEGF; Bernardini, et al. *J. Urol.*, 2001, 166(4): 1275-9; Starnes, et al. *J. Thorac. Cardiovasc. Surg.*, 2001, 122(3): 518-23; Dias, et al. *Blood*, 2002, 99: 2179-2184), the VEGF receptor (i.e., VEGF-R, flk-1/KDR; Starnes, et al. *J. Thorac. Cardiovasc. Surg.*, 2001, 122(3): 518-23), EPH receptors (i.e., EPHA2; Gerety, et al. 1999, *Cell*, 4: 403-414), epidermal growth factor receptor (i.e., EGFR; Ciardcillo, et al. Clin. Cancer Res., 2001, 7(10): 2958-70), basic fibroblast growth factor (i.e., bFGF; Davidson, et al. Clin. Exp. Metastasis 2000,18(6): 501-7; Poon, et al. Am J. Surg., 2001, 182(3):298-304), platelet-derived cell growth factor (i.e., PDGF-B), platelet-derived endothelial cell growth factor (PD-ECGF; Hong, et al. J. Mol. Med., 2001, 8(2):141-8), transforming growth factors (i.e., TGF-α; Hong, et al. J. Mol. Med., 2001, 8(2):141-8), endoglin (Balza, et al. *Int. J. Cancer*, 2001, 94: 579-585), Id proteins (Benezra, R. Trends Cardiovasc. Med., 2001, 11(6):237-41), proteases such as uPA, uPAR, and matrix metalloproteinases (MMP-2, MMP-9; Djonov, et al. J. Pathol., 2001, 195(2):147-55), nitric oxide synthase (Am. J. Ophthalmol., 2001, 132(4):551-6), aminopeptidase (Rouslhati, E. Nature Cancer, 2: 84-90, 2002), thrombospondins (i.e., TSP-1, TSP-2; Alvarez, et al. Gynecol. Oncol., 2001, 82(2):273-8; Seki, et al. Int. J. Oncol., 2001, 19(2):305-10), k-*ras* (Zhang, et al. Cancer Res., 2001, 61(16):6050-4), *Wnt* (Zhang, et al. Cancer Res., 2001, 61(16):6050-4), cyclin-dependent kinases (CDKs; Drug Resist. Updat. 2000, 3(2):83-88), microtubules (Timar, et al. 2001. *Path. Oncol. Res.*, 7(2): 85-94), heat shock proteins (i.e., HSP90 (Timar, *supra*)), heparin-binding factors (i.e., heparinase; Gohji, et al. Int. J. Cancer, 2001, 95(5):295-301), synthases (i.e., ATP synthase,

thymidilate synthase), collagen receptors, integrins (i.e., αυβ3, αυβ5, α1β1, α2β1, α5β1), the surface proteolglycan NG2, AAC2-1, or AAC2-2, among others, including "wild-type" (i.e., normally encoded by the genome, naturally-occurring), modified, mutated versions as well as other fragments and derivatives thereof. Any of these targets may be suitable in practicing the present invention, either alone or in combination with one another or with other agents.

The nucleic acid molecule may comprise or consist of a nucleotide sequence encoding one or more immunogenic targets, or fragments or derivatives thereof, such as that contained in a DNA insert in an ATCC Deposit. The term "nucleic acid sequence" or "nucleic acid molecule" refers to a DNA or RNA sequence. The term encompasses molecules formed from any of the known base analogs of DNA and RNA such as, but not limited to 4-acetylcytosine, 8-hydroxy-N6-methyladenosine, aziridinyl-cytosine, pseudoisocytosine, 5-(carboxyhydroxylmethyl) uracil, 5-fluorouracil, 5-bromouracil, 5-carboxymethylaminomethyl-2-thiouracil, 5-carboxy-methylaminomethyluracil, dihydrouracil, inosine, N6-iso-pentenyladenine, 1-methyladenine, 1-methylpseudouracil, 1-methylguanine, 1-methylinosine, 2,2-dimethyl-guanine, 2-methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N6-methyladenine, 7-methylguanine, 5-methylaminomethyluracil, 5-methoxyamino-methyl-2-thiouracil, beta-D-mannosylqueosine, 5' -methoxycarbonyl-methyluracil, 5-methoxyuracil, 2-methylthio-N6-isopentenyladenine, uracil-5-oxyacetic acid methylester, uracil-5-oxyacetic acid, oxybutoxosine, pseudouracil, queosine, 2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, N-uracil-5-oxyacetic acid methylester, uracil-5-oxyacetic acid, pseudouracil, queosine, 2-thiocytosine, and 2,6-diaminopurine, among others.

An isolated nucleic acid molecule is one that: (1) is separated from at least about 50 percent of proteins, lipids, carbohydrates, or other materials with which it is naturally found when total nucleic acid is isolated from the source cells; (2) is not be linked to all or a portion of a polynucleotide to which the nucleic acid molecule is linked in nature; (3) is operably linked to a polynucleotide which it is not linked to in nature; and / or, (4) does not occur in nature as part of a larger polynucleotide sequence. Preferably, the isolated nucleic acid molecule of the present invention is substantially free from any other contaminating nucleic acid molecule(s) or other contaminants that are found in its natural environment that would interfere with its use in polypeptide production or its therapeutic, diagnostic, prophylactic or research use. As used herein, the term "naturally occurring" or "native" or "naturally found" when used in connection

with biological materials such as nucleic acid molecules, polypeptides, host cells, and the like, refers to materials which are found in nature and are not manipulated by man. Similarly, "non-naturally occurring" or "non-native" as used herein refers to a material that is not found in nature or that has been structurally modified or synthesized by man.

The identity of two or more nucleic acid or amino acid sequences is determined by comparing the sequences. As known in the art, "identity" means the degree of sequence relatedness between nucleic acid or amino acid sequences as determined by the match between the units making up the molecules (i.e., nucleotides or amino acid residues). Identity measures the percent of identical matches between the smaller of two or more sequences with gap alignments (if any) addressed by a particular mathematical model or computer program (i.e., an algorithm). Identity between nucleic acid sequences may also be determined by the ability of the nucleic acid sequences to hybridize to one another. In defining the process of hybridization, the term "highly stringent conditions" and "moderately stringent conditions" refer to conditions that permit hybridization of nucleic acid strands whose sequences are complementary, and to exclude hybridization of significantly mismatched nucleic acids. Examples of "highly stringent conditions" for hybridization and washing are 0.015 M sodium chloride, 0.0015 M sodium citrate at 65-68°C or 0.015 M sodium chloride, 0.0015 M sodium citrate, and 50% formamide at 42°C. (see, for example, Sambrook, Fritsch & Maniatis, *Molecular Cloning: A Laboratory Manual* (2nd ed., Cold Spring Harbor Laboratory, 1989); Anderson *et al.*, *Nucleic Acid Hybridisation: A Practical Approach* Ch. 4 (IRL Press Limited)). The term "moderately stringent conditions" refers to conditions under which a DNA duplex with a greater degree of base pair mismatching than could occur under "highly stringent conditions" is able to form. Exemplary moderately stringent conditions are 0.015 M sodium chloride, 0.0015 M sodium citrate at 50-65°C or 0.015 M sodium chloride, 0.0015 M sodium citrate, and 20% formamide at 37-50°C. By way of example, moderately stringent conditions of 50°C in 0.015 M sodium ion will allow about a 21% mismatch. During hybridization, other agents may be included in the hybridization and washing buffers for the purpose of reducing non-specific and/or background hybridization. Examples are 0.1% bovine serum albumin, 0.1% polyvinyl-pyrrolidone, 0.1% sodium pyrophosphate, 0.1% sodium dodecylsulfate, $NaDodSO_4$, (SDS), ficoll, Denhardt's solution, sonicated salmon sperm DNA (or another non-complementary DNA), and dextran sulfate, although other suitable agents can also be used. The concentration and types of these

additives can be changed without substantially affecting the stringency of the hybridization conditions.. Hybridization experiments are usually carried out at pH 6.8-7.4; however, at typical ionic strength conditions, the rate of hybridization is nearly independent of pH.

In preferred embodiments of the present invention, vectors are used to transfer a nucleic acid sequence encoding an immunogenic target to a cell. A vector is any molecule used to transfer a nucleic acid sequence to a host cell. In certain cases, an expression vector is utilized. An expression vector is a nucleic acid molecule that is suitable for transformation of a host cell and contains nucleic acid sequences that direct and / or control the expression of the transferred nucleic acid sequences. Expression includes, but is not limited to, processes such as transcription, translation, and splicing, if introns are present. Expression vectors typically comprise one or more flanking sequences operably linked to a heterologous nucleic acid sequence encoding a polypeptide. Flanking sequences may be homologous (i.e., from the same species and / or strain as the host cell), heterologous (i.e., from a species other than the host cell species or strain), hybrid (i.e., a combination of flanking sequences from more than one source), or synthetic, for example.

A flanking sequence is preferably capable of effecting the replication, transcription and / or translation of the coding sequence and is operably linked to a coding sequence. As used herein, the term operably linked refers to a linkage of polynucleotide elements in a functional relationship. For instance, a promoter or enhancer is operably linked to a coding sequence if it affects the transcription of the coding sequence. However, a flanking sequence need not necessarily be contiguous with the coding sequence, so long as it functions correctly. Thus, for example, intervening untranslated yet transcribed sequences can be present between a promoter sequence and the coding sequence and the promoter sequence may still be considered operably linked to the coding sequence. Similarly, an enhancer sequence may be located upstream or downstream from the coding sequence and affect transcription of the sequence.

In certain embodiments, it is preferred that the flanking sequence is a transcriptional regulatory region that drives high-level gene expression in the target cell. The transcriptional regulatory region may comprise, for example, a promoter, enhancer, silencer, repressor element, or combinations thereof. The transcriptional regulatory region may be either constitutive, tissue-specific, cell-type specific (i.e., the region is drives higher levels of transcription in a one type of tissue or cell as compared to another), or regulatable (i.e., responsive to interaction with a

compound such as tetracycline). The source of a transcriptional regulatory region may be any prokaryotic or eukaryotic organism, any vertebrate or invertebrate organism, or any plant, provided that the flanking sequence functions in a cell by causing transcription of a nucleic acid within that cell. A wide variety of transcriptional regulatory regions may be utilized in practicing the present invention.

Suitable transcriptional regulatory regions include the CMV promoter (i.e., the CMV-immediate early promoter); promoters from eukaryotic genes (i.e., the estrogen-inducible chicken ovalbumin gene, the interferon genes, the gluco-corticoid-inducible tyrosine aminotransferase gene, and the thymidine kinase gene); and the major early and late adenovirus gene promoters; the SV40 early promoter region (Bernoist and Chambon, 1981, *Nature* 290:304-10); the promoter contained in the 3' long terminal repeat (LTR) of Rous sarcoma virus (RSV) (Yamamoto, *et al.*, 1980, *Cell* 22:787-97); the herpes simplex virus thymidine kinase (HSV-TK) promoter (Wagner *et al.*, 1981, *Proc. Natl. Acad. Sci. U.S.A.* 78:1444-45); the regulatory sequences of the metallothionine gene (Brinster *et al.*, 1982, *Nature* 296:39-42); prokaryotic expression vectors such as the beta-lactamase promoter (Villa-Kamaroff *et al.*, 1978, *Proc. Natl. Acad. Sci. U.S.A.*, 75:3727-31); or the tac promoter (DeBoer *et al.*, 1983, *Proc. Natl. Acad. Sci. U.S.A.*, 80:21-25). Tissue- and / or cell-type specific transcriptional control regions include, for example, the elastase I gene control region which is active in pancreatic acinar cells (Swift *et al.*, 1984, *Cell* 38:639-46; Ornitz *et al.*, 1986, *Cold Spring Harbor Symp. Quant. Biol.* 50:399-409 (1986); MacDonald, 1987, *Hepatology* 7:425-515); the insulin gene control region which is active in pancreatic beta cells (Hanahan, 1985, *Nature* 315:115-22); the immunoglobulin gene control region which is active in lymphoid cells (Grosschedl *et al.*, 1984, *Cell* 38:647-58; Adames *et al.*, 1985, *Nature* 318:533-38; Alexander *et al.*, 1987, *Mol. Cell. Biol.*, 7:1436-44); the mouse mammary tumor virus control region in testicular, breast, lymphoid and mast cells (Leder *et al.*, 1986, *Cell* 45:485-95); the albumin gene control region in liver (Pinkert *et al.*, 1987, *Genes and Devel.* 1:268-76); the alpha-feto-protein gene control region in liver (Krumlauf *et al.*, 1985, *Mol. Cell. Biol.*, 5:1639-48; Hammer *et al.*, 1987, *Science* 235:53-58); the alpha 1-antitrypsin gene control region in liver (Kelsey *et al.*, 1987, *Genes and Devel.* 1:161-71); the beta-globin gene control region in myeloid cells (Mogram *et al.*, 1985, *Nature* 315:338-40; Kollias *et al.*, 1986, *Cell* 46:89-94); the myelin basic protein gene control region in oligodendrocyte cells in the brain (Readhead *et al.*, 1987, *Cell* 48:703-12); the myosin light chain-2 gene control region in

skeletal muscle (Sani, 1985, *Nature* 314:283-86); the gonadotropic releasing hormone gene control region in the hypothalamus (Mason *et al.*, 1986, *Science* 234:1372-78), and the tyrosinase promoter in melanoma cells (Hart, I. Semin Oncol 1996 Feb;23(1):154-8; Siders, et al. Cancer Gene Ther 1998 Sep-Oct;5(5):281-91), among others. Inducible promoters that are activated in the presence of a certain compound or condition such as light, heat, radiation, tetracycline, or heat shock proteins, for example, may also be utilized (see, for example, WO 00/10612). Other suitable promoters are known in the art.

As described above, enhancers may also be suitable flanking sequences. Enhancers are cis-acting elements of DNA, usually about 10-300 bp in length, that act on the promoter to increase transcription. Enhancers are typically orientation- and position-independent, having been identified both 5' and 3' to controlled coding sequences. Several enhancer sequences available from mammalian genes are known (i.e., globin, elastase, albumin, alpha-feto-protein and insulin). Similarly, the SV40 enhancer, the cytomegalovirus early promoter enhancer, the polyoma enhancer, and adenovirus enhancers are useful with eukaryotic promoter sequences. While an enhancer may be spliced into the vector at a position 5' or 3' to nucleic acid coding sequence, it is typically located at a site 5' from the promoter. Other suitable enhancers are known in the art, and would be applicable to the present invention.

While preparing reagents of the present invention, cells may need to be transfected or transformed. Transfection refers to the uptake of foreign or exogenous DNA by a cell, and a cell has been transfected when the exogenous DNA has been introduced inside the cell membrane. A number of transfection techniques are well known in the art (i.e., Graham *et al.*, 1973, *Virology* 52:456; Sambrook *et al.*, *Molecular Cloning, A Laboratory Manual* (Cold Spring Harbor Laboratories, 1989); Davis *et al.*, *Basic Methods in Molecular Biology* (Elsevier, 1986); and Chu *et al.*, 1981, *Gene* 13:197). Such techniques can be used to introduce one or more exogenous DNA moieties into suitable host cells.

In certain embodiments, it is preferred that transfection of a cell results in transformation of that cell. A cell is transformed when there is a change in a characteristic of the cell, being transformed when it has been modified to contain a new nucleic acid. Following transfection, the transfected nucleic acid may recombine with that of the cell by physically integrating into a chromosome of the cell, may be maintained transiently as an episomal element without being

replicated, or may replicate independently as a plasmid. A cell is stably transformed when the nucleic acid is replicated with the division of the cell.

The expression vectors of the present invention also provide for expression of fragments of immunogenic targets. Fragments may include sequences truncated at the amino terminus (with or without a leader sequence) and / or the carboxy terminus. Fragments may also include variants (i.e., allelic, splice), orthologs, homologues, and other variants having one or more amino acid additions or substitutions or internal deletions as compared to the parental sequence. In preferred embodiments, truncations and/or deletions comprise about 1-5 amino acids, 5-10 amino acids, 10-20 amino acids, 20-30 amino acids, 30-40 amino acids, 40-50 amino acids, or more. Such polypeptide fragments may optionally comprise an amino terminal methionine residue. It will be appreciated that such fragments can be used, for example, to generate antibodies or cellular immune responses to immunogenic targets.

A variant is a sequence having one or more sequence substitutions, deletions, and/or additions as compared to the subject sequence. Variants may be naturally occurring or artificially constructed. Such variants may be prepared from the corresponding nucleic acid molecules. In preferred embodiments, the variants have from 1 to 3, or from 1 to 5, or from 1 to 10, or from 1 to 15, or from 1 to 20, or from 1 to 25, or from 1 to 30, or from 1 to 40, or from 1 to 50, or more than 50 amino acid substitutions, insertions, additions and/or deletions.

An allelic variant is one of several possible naturally-occurring alternate forms of a sequence occupying a given locus on a chromosome of an organism or a population of organisms. A splice variant is a polypeptide generated from one of several RNA transcript resulting from splicing of a primary transcript. An ortholog is a similar nucleic acid or polypeptide sequence from another species. For example, the mouse and human versions of an immunogenic target may be considered orthologs of each other. A derivative of a sequence is one that is derived from a parental sequence those sequences having substitutions, additions, deletions, or chemically modified variants. Variants may also include fusion proteins, which refers to the fusion of one or more first sequences (such as a peptide) at the amino or carboxy terminus of at least one other sequence (such as a heterologous peptide).

"Similarity" is a concept related to identity, except that similarity refers to a measure of relatedness which includes both identical matches and conservative substitution matches. If two polypeptide sequences have, for example, 10/20 identical amino acids, and the remainder are all

non-conservative substitutions, then the percent identity and similarity would both be 50%. If in the same example, there are five more positions where there are conservative substitutions, then the percent identity remains 50%, but the percent similarity would be 75% (15/20). Therefore, in cases where there are conservative substitutions, the percent similarity between two polypeptides will be higher than the percent identity between those two polypeptides.

Substitutions may be conservative, or non-conservative, or any combination thereof. Conservative amino acid modifications to the sequence of a polypeptide (and the corresponding modifications to the encoding nucleotides) may produce polypeptides having functional and chemical characteristics similar to those of a parental polypeptide. For example, a "conservative amino acid substitution" may involve a substitution of a native amino acid residue with a non-native residue such that there is little or no effect on the size, polarity, charge, hydrophobicity, or hydrophilicity of the amino acid residue at that position and, in particlar, does not result in decreased immunogenicity. Suitable conservative amino acid substitutions are shown in **Table I**.

Table I

Original Residues	Exemplary Substitutions	Preferred Substitutions
Ala	Val, Leu, Ile	Val
Arg	Lys, Gln, Asn	Lys
Asn	Gln	Gln
Asp	Glu	Glu
Cys	Ser, Ala	Ser
Gln	Asn	Asn
Glu	Asp	Asp
Gly	Pro, Ala	Ala
His	Asn, Gln, Lys, Arg	Arg
Ile	Leu, Val, Met, Ala, Phe, Norleucine	Leu
Leu	Norleucine, Ile, Val, Met, Ala, Phe	Ile
Lys	Arg, 1,4 Diamino-butyric Acid, Gln, Asn	Arg
Met	Leu, Phe, Ile	Leu
Phe	Leu, Val, Ile, Ala, Tyr	Leu
Pro	Ala	Gly
Ser	Thr, Ala, Cys	Thr
Thr	Ser	Ser
Trp	Tyr, Phe	Tyr
Tyr	Trp, Phe, Thr, Ser	Phe
Val	Ile, Met, Leu, Phe, Ala, Norleucine	Leu

A skilled artisan will be able to determine suitable variants of an immunogenic target using well-known techniques. For identifying suitable areas of the molecule that may be changed without destroying biological activity (i.e., MHC binding, immunogenicity), one skilled in the art may target areas not believed to be important for that activity. For example, when immunogenic targets with similar activities from the same species or from other species are known, one skilled in the art may compare the amino acid sequence of a polypeptide to such similar polypeptides. By performing such analyses, one can identify residues and portions of the molecules that are conserved. It will be appreciated that changes in areas of the molecule that are not conserved relative to such similar immunogenic targets would be less likely to adversely affect the biological activity and/or structure of a polypeptide. Similarly, the residues required for binding to MHC are known, and may be modified to improve binding. However, modifications resulting in decreased binding to MHC will not be appropriate in most situations. One skilled in the art would also know that, even in relatively conserved regions, one may substitute chemically similar amino acids for the naturally occurring residues while retaining activity. Therefore, even areas that may be important for biological activity or for structure may be subject to conservative amino acid substitutions without destroying the biological activity or without adversely affecting the structure of the immunogenic target.

Other preferred polypeptide variants include glycosylation variants wherein the number and/or type of glycosylation sites have been altered compared to the subject amino acid sequence. In one embodiment, polypeptide variants comprise a greater or a lesser number of N-linked glycosylation sites than the subject amino acid sequence. An N-linked glycosylation site is characterized by the sequence Asn-X-Ser or Asn-X-Thr, wherein the amino acid residue designated as X may be any amino acid residue except proline. The substitution of amino acid residues to create this sequence provides a potential new site for the addition of an N-linked carbohydrate chain. Alternatively, substitutions that eliminate this sequence will remove an existing N-linked carbohydrate chain. Also provided is a rearrangement of N-linked carbohydrate chains wherein one or more N-linked glycosylation sites (typically those that are naturally occurring) are eliminated and one or more new N-linked sites are created. To affect O-linked glycosylation of a polypeptide, one would modify serine and / or threonine residues.

Additional preferred variants include cysteine variants, wherein one or more cysteine residues are deleted or substituted with another amino acid (*e.g.*, serine) as compared to the subject amino acid sequence set. Cysteine variants are useful when peptides or polypeptides must be refolded into a biologically active conformation such as after the isolation of insoluble inclusion bodies. Cysteine variants generally have fewer cysteine residues than the native protein, and typically have an even number to minimize interactions resulting from unpaired cysteines.

In other embodiments, the peptides or polypeptides may be attached to one or more fusion segments that assist in purification of the polypeptides. Fusions can be made either at the amino terminus or at the carboxy terminus of the subject polypeptide variant thereof. Fusions may be direct with no linker or adapter molecule or may be through a linker or adapter molecule. A linker or adapter molecule may be one or more amino acid residues, typically from about 20 to about 50 amino acid residues. A linker or adapter molecule may also be designed with a cleavage site for a DNA restriction endonuclease or for a protease to allow for the separation of the fused moieties. It will be appreciated that once constructed, the fusion polypeptides can be derivatized according to the methods described herein. Suitable fusion segments include, among others, metal binding domains (e.g., a poly-histidine segment), immunoglobulin binding domains (i.e., Protein A, Protein G, T cell, B cell, Fc receptor, or complement protein antibody-binding domains), sugar binding domains (e.g., a maltose binding domain), and/or a "tag" domain (i.e., at least a portion of α-galactosidase, a strep tag peptide, a T7 tag peptide, a FLAG peptide, or other domains that can be purified using compounds that bind to the domain, such as monoclonal antibodies). This tag is typically fused to the peptide or polypeptide and upon expression may serve as a means for affinity purification of the sequence of interest polypeptide from the host cell. Affinity purification can be accomplished, for example, by column chromatography using antibodies against the tag as an affinity matrix. Optionally, the tag can subsequently be removed from the purified sequence of interest polypeptide by various means such as using certain peptidases for cleavage. As described below, fusions may also be made between a TA and a co-stimulatory components such as the chemokines CXC10 (IP-10), CCL7 (MCP-3), or CCL5 (RANTES), for example.

A fusion motif may enhance transport of an immunogenic target to an MHC processing compartment, such as the endoplasmic reticulum. These sequences, referred to as tranduction or

transcytosis sequences, include sequences derived from HIV tat (see Kim et al. 1997 J. Immunol. 159:1666), *Drosophila* antennapedia (see Schutze-Redelmeier et al. 1996 J. Immunol. 157:650), or human period-1 protein (hPER1; in particular, SRRHHCRSKAKRSRHH).

In addition, the polypeptide or variant thereof may be fused to a homologous peptide or polypeptide to form a homodimer or to a heterologous peptide or polypeptide to form a heterodimer. Heterologous peptides and polypeptides include, but are not limited to an epitope to allow for the detection and/or isolation of a fusion polypeptide; a transmembrane receptor protein or a portion thereof, such as an extracellular domain or a transmembrane and intracellular domain; a ligand or a portion thereof which binds to a transmembrane receptor protein; an enzyme or portion thereof which is catalytically active; a polypeptide or peptide which promotes oligomerization, such as a leucine zipper domain; a polypeptide or peptide which increases stability, such as an immunoglobulin constant region; a peptide or polypeptide which has a therapeutic activity different from the peptide or polypeptide; and/or variants thereof.

In certain embodiments, it may be advantageous to combine a nucleic acid sequence encoding an immunogenic target with one or more co-stimulatory component(s) such as cell surface proteins, cytokines or chemokines in a composition of the present invention. The co-stimulatory component may be included in the composition as a polypeptide or as a nucleic acid encoding the polypeptide, for example. Suitable co-stimulatory molecules include, for instance, polypeptides that bind members of the CD28 family (i.e., CD28, ICOS; Hutloff, et al. *Nature* 1999, 397: 263–265; Peach, et al. *J Exp Med* 1994, 180: 2049–2058) such as the CD28 binding polypeptides B7.1 (CD80; Schwartz, 1992; Chen et al; 1992; Ellis, et al. *J. Immunol.*, 156(8): 2700-9), B7.2 (CD86; Ellis, et al. *J. Immunol.*, 156(8): 2700-9), and mutants / variants thereof (WO 00/66162); polypeptides which bind members of the integrin family (i.e., LFA-1 (CD11a / CD18); Sedwick, et al. *J Immunol* 1999, 162: 1367–1375; Wülfing, et al. *Science* 1998, 282: 2266–2269; Lub, et al. *Immunol Today* 1995, 16: 479–483) including members of the ICAM family (i.e., ICAM-1, -2 or -3); polypeptides which bind CD2 family members (i.e., CD2, signalling lymphocyte activation molecule (CDw150 or "SLAM"; Aversa, et al. *J Immunol* 1997, 158: 4036–4044)) such as CD58 (LFA-3; CD2 ligand; Davis, et al. *Immunol Today* 1996, 17: 177–187) or SLAM ligands (Sayos, et al. *Nature* 1998, 395: 462–469); polypeptides which bind heat stable antigen (HSA or CD24; Zhou, et al. *Eur J Immunol* 1997, 27: 2524–2528); polypeptides which bind to members of the TNF receptor (TNFR) family (i.e.,

4-1BB (CD137; Vinay, et al. *Semin Immunol* 1998, 10: 481–489), OX40 (CD134; Weinberg, et al. *Semin Immunol* 1998, 10: 471–480; Higgins, et al. *J Immunol* 1999, 162: 486–493), and CD27 (Lens, et al. *Semin Immunol* 1998, 10: 491–499)) such as 4-1BBL (4-1BB ligand; Vinay, et al. *Semin Immunol* 1998, 10: 481–48; DeBenedette, et al. *J Immunol* 1997, 158: 551–559), TNFR associated factor-1 (TRAF-1; 4-1BB ligand; Saoulli, et al. *J Exp Med* 1998, 187: 1849–1862, Arch, et al. *Mol Cell Biol* 1998, 18: 558–565), TRAF-2 (4-1BB and OX40 ligand; Saoulli, et al. *J Exp Med* 1998, 187: 1849–1862; Oshima, et al. *Int Immunol* 1998, 10: 517–526, Kawamata, et al. *J Biol Chem* 1998, 273: 5808–5814), TRAF-3 (4-1BB and OX40 ligand; Arch, et al. *Mol Cell Biol* 1998, 18: 558–565; Jang, et al. *Biochem Biophys Res Commun* 1998, 242: 613–620; Kawamata S, et al. *J Biol Chem* 1998, 273: 5808–5814), OX40L (OX40 ligand; Gramaglia, et al. *J Immunol* 1998, 161: 6510–6517), TRAF-5 (OX40 ligand; Arch, et al. *Mol Cell Biol* 1998, 18: 558–565; Kawamata, et al. *J Biol Chem* 1998, 273: 5808–5814), and CD70 (CD27 ligand; Couderc, et al. *Cancer Gene Ther.*, 5(3): 163-75). CD154 (CD40 ligand or "CD40L"; Gurunathan, et al. *J. Immunol.*, 1998, 161: 4563-4571; Sine, et al. *Hum. Gene Ther.*, 2001, 12: 1091-1102) may also be suitable.

One or more cytokines may also be suitable co-stimulatory components or "adjuvants", either as polypeptides or being encoded by nucleic acids contained within the compositions of the present invention (Parmiani, et al. Immunol Lett 2000 Sep 15; 74(1): 41-4; Berzofsky, et al. Nature Immunol. 1: 209-219). Suitable cytokines include, for example, interleukin-2 (IL-2) (Rosenberg, et al. *Nature Med.* 4: 321-327 (1998)), IL-4, IL-7, IL-12 (reviewed by Pardoll, 1992; Harries, et al. J. Gene Med. 2000 Jul-Aug;2(4):243-9; Rao, et al. *J. Immunol.* 156: 3357-3365 (1996)), IL-15 (Xin, et al. *Vaccine*, 17:858-866, 1999), IL-16 (Cruikshank, et al. J. Leuk Biol. 67(6): 757-66, 2000), IL-18 (*J. Cancer Res. Clin. Oncol.* 2001. 127(12): 718-726), GM-CSF (CSF (Disis, et al. *Blood*, 88: 202-210 (1996)), tumor necrosis factor-alpha (TNF-α), or interferons such as IFN-α or INF-γ. Other cytokines may also be suitable for practicing the present invention, as is known in the art.

Chemokines may also be utilized, in either polypeptide or nucleic acid form. Fusion proteins comprising CXCL10 (IP-10) and CCL7 (MCP-3) fused to a tumor self-antigen have been shown to induce anti-tumor immunity (Biragyn, et al. *Nature Biotech.* 1999, 17: 253-258). The chemokines CCL3 (MIP-1α) and CCL5 (RANTES) (Boyer, et al. *Vaccine*, 1999, 17 (Supp.

2): S53-S64) may also be of use in practicing the present invention. Other suitable chemokines are known in the art.

It is also known in the art that suppressive or negative regulatory immune mechanisms may be blocked, resulting in enhanced immune responses. For instance, treatment with anti-CTLA-4 (Shrikant, et al. *Immunity*, 1996, 14: 145-155; Sutmuller, et al. *J. Exp. Med.*, 2001, 194: 823-832), anti-CD25 (Sutmuller, *supra*), anti-CD4 (Matsui, et al. *J. Immunol.*, 1999, 163: 184-193), the fusion protein IL13Ra2-Fc (Terabe, et al. *Nature Immunol.*, 2000, 1: 515-520), and combinations thereof (i.e., anti-CTLA-4 and anti-CD25, Sutmuller, *supra*) have been shown to upregulate anti-tumor immune responses and would be suitable in practicing the present invention. Such treatments, among others, may also be combined with the one or more immunogenic targets of the present invention.

Any of these components may be used alone or in combination with other agents. For instance, it has been shown that a combination of CD80, ICAM-1 and LFA-3 ("TRICOM") may potentiate anti-cancer immune responses (Hodge, et al. *Cancer Res.* 59: 5800-5807 (1999). Other effective combinations include, for example, IL-12 + GM-CSF (Ahlers, et al. *J. Immunol.*, 158: 3947-3958 (1997); Iwasaki, et al. *J. Immunol.* 158: 4591-4601 (1997)), IL-12 + GM-CSF + TNF-α (Ahlers, et al. *Int. Immunol.* 13: 897-908 (2001)), CD80 + IL-12 (Fruend, et al. *Int. J. Cancer*, 85: 508-517 (2000); Rao, et al. *supra*), and CD86 + GM-CSF + IL-12 (Iwasaki, supra). One of skill in the art would be aware of additional combinations useful in carrying out the present invention. In addition, the skilled artisan would be aware of additional reagents or methods that may be used to modulate such mechanisms. These reagents and methods, as well as others known by those of skill in the art, may be utilized in practicing the present invention.

Additional strategies for improving the efficiency of nucleic acid-based immunization may also be used including, for example, the use of self-replicating viral replicons (Caley, et al. 1999. *Vaccine*, 17: 3124-2135; Dubensky, et al. 2000. *Mol. Med.* 6: 723-732; Leitner, et al. 2000. *Cancer Res.* 60: 51-55), codon optimization (Liu, et al. 2000. *Mol. Ther.*, 1: 497-500; Dubensky, *supra*; Huang, et al. 2001. *J. Virol.* 75: 4947-4951), *in vivo* electroporation (Widera, et al. 2000. *J. Immunol.* 164: 4635-3640), incorporation of CpG stimulatory motifs (Gurunathan, et al. *Ann. Rev. Immunol.*, 2000, 18: 927-974; Leitner, *supra*; Cho, et al. J. Immunol. 168(10):4907-13), sequences for targeting of the endocytic or ubiquitin-processing pathways (Thomson, et al. 1998. *J. Virol.* 72: 2246-2252; Velders, et al. 2001. *J. Immunol.*

166: 5366-5373), Marek's disease virus type 1 VP22 sequences (J. Virol. 76(6):2676-82, 2002), prime-boost regimens (Gurunathan, *supra*; Sullivan, et al. 2000. *Nature*, 408: 605-609; Hanke, et al. 1998. *Vaccine*, 16: 439-445; Amara, et al. 2001. *Science*, 292: 69-74), and the use of mucosal delivery vectors such as *Salmonella* (Darji, et al. 1997. *Cell*, 91: 765-775; Woo, et al. 2001. *Vaccine*, 19: 2945-2954). Other methods are known in the art, some of which are described below.

Chemotherapeutic agents, radiation, anti-angiogenic compounds, or other agents may also be utilized in treating and / or preventing cancer using immunogenic targets (Sebti, et al. Oncogene 2000 Dec 27;19(56):6566-73). For example, in treating metastatic melanoma, suitable chemotherapeutic regimens may include BELD (bleomycin, vindesine, lomustine, and deacarbazine; Young, et al. 1985. Cancer, 55: 1879-81), BOLD (bleomycin, vincristine, lomustine, dacarbazine; Seigler, et al. 1980. Cancer, 46 : 2346-8) ; DD (dacarbazine, actinomycin ; Hochster, et al. Cancer Treatment Reports, 69: 39-42), or POC (procarbazine, vincristine, lomustine; Carmo-Pereira, et al. 1984. Cancer Treatment Reports, 68: 1211-4) among others. Other suitable chemotherapeutic regimens may also be utilized.

Many anti-angiogenic agents are known in the art and would be suitable for co-administration with the immunogenic target vaccines and/or chemotherapeutic regimens (see, for example, Timar, et al. 2001. *Pathology Oncol. Res.*, 7(2): 85-94). Such agents include, for example, physiological agents such as growth factors (i.e., ANG-2, NK1,2,4 (HGF), transforming growth factor beta (TGF-β)), cytokines (i.e., interferons such as IFN-α, -β, -γ, platelet factor 4 (PF-4), PR-39), proteases (i.e., cleaved AT-III, collagen XVIII fragment (Endostatin)), HmwKallikrein-d5 plasmin fragment (Angiostatin), prothrombin-F1-2, TSP-1), protease inhibitors (i.e., tissue inhibitor of metalloproteases such as TIMP-1, -2, or –3; maspin; plasminogen activator-inhibitors such as PAI-1; pigment epithelium derived factor (PEDF)), Tumstatin (available through ILEX, Inc.), antibody products (i.e., the collagen-binding antibodies HUIV26, HUI77, XL313; anti-VEGF; anti-integrin (i.e., Vitaxin, (Lxsys))), and glycosidases (i.e., heparinase-I, -III). "Chemical" or modified physiological agents known or believed to have anti-angiogenic potential include, for example, vinblastine, taxol, ketoconazole, thalidomide, dolestatin, combrestatin A, rapamycin (Guba, et al. 2002, *Nature Med.*, 8: 128-135), CEP-7055 (available from Cephalon, Inc.), flavone acetic acid, Bay 12-9566 (Bayer Corp.), AG3340 (Agouron, Inc.), CGS 27023A (Novartis), tetracylcine derivatives (i.e., COL-3

(Collagenix, Inc.)), Neovastat (Aetema), BMS-275291 (Bristol-Myers Squibb), low dose 5-FU, low dose methotrexate (MTX), irsofladine, radicicol, cyclosporine, captopril, celecoxib, D45152-sulphated polysaccharide, cationic protein (Protamine), cationic peptide-VEGF, Suramin (polysulphonated napthyl urea), compounds that interfere with the function or production of VEGF (i.e., SU5416 or SU6668 (Sugen), PTK787/ZK22584 (Novartis)), Distamycin A, Angiozyme (ribozyme), isoflavinoids, staurosporine derivatives, genistein, EMD121974 (Merck KcgaA), tyrphostins, isoquinolones, retinoic acid, carboxyamidotriazole, TNP-470, octreotide, 2-methoxyestradiol, aminosterols (i.e., squalamine), glutathione analogues (i.e., N-acteyl-L-cysteine), combretastatin A-4 (Oxigene), Eph receptor blocking agents (*Nature*, 414:933-938, 2001), Rh-Angiostatin, Rh-Endostatin (WO 01/93897), cyclic-RGD peptide, accutin-disintegrin, benzodiazepenes, humanized anti-avb3 Ab, Rh-PAI-2, amiloride, p-amidobenzamidine, anti-uPA ab, anti-uPAR Ab, L-phanylalanin-N-methylamides (i.e., Batimistat, Marimastat), AG3340, and minocycline. Many other suitable agents are known in the art and would suffice in practicing the present invention.

The present invention may also be utilized in combination with "non-traditional" methods of treating cancer. For example, it has recently been demonstrated that administration of certain anaerobic bacteria may assist in slowing tumor growth. In one study, *Clostridium novyi* was modified to eliminate a toxin gene carried on a phage episome and administered to mice with colorectal tumors (Dang, et al. *P.N.A.S. USA*, 98(26): 15155-15160, 2001). In combination with chemotherapy, the treatment was shown to cause tumor necrosis in the animals. The reagents and methodologies described in this application may be combined with such treatment methodologies.

Nucleic acids encoding immunogenic targets may be administered to patients by any of several available techniques. Various viral vectors that have been successfully utilized for introducing a nucleic acid to a host include retrovirus, adenovirus, adeno-associated virus (AAV), herpes virus, and poxvirus, among others. It is understood in the art that many such viral vectors are available in the art. The vectors of the present invention may be constructed using standard recombinant techniques widely available to one skilled in the art. Such techniques may be found in common molecular biology references such as *Molecular Cloning: A Laboratory Manual* (Sambrook, et al., 1989, Cold Spring Harbor Laboratory Press), *Gene Expression Technology* (Methods in Enzymology, Vol. 185, edited by D. Goeddel, 1991. Academic Press,

San Diego, CA), and *PCR Protocols: A Guide to Methods and Applications* (Innis, et al. 1990. Academic Press, San Diego, CA).

Preferred retroviral vectors are derivatives of lentivirus as well as derivatives of murine or avian retroviruses. Examples of suitable retroviral vectors include, for example, Moloney murine leukemia virus (MoMuLV), Harvey murine sarcoma virus (HaMuSV), murine mammary tumor virus (MuMTV), SIV, BIV, HIV and Rous Sarcoma Virus (RSV). A number of retroviral vectors can incorporate multiple exogenous nucleic acid sequences. As recombinant retroviruses are defective, they require assistance in order to produce infectious vector particles. This assistance can be provided by, for example, helper cell lines encoding retrovirus structural genes. Suitable helper cell lines include Ψ2, PA317 and PA12, among others. The vector virions produced using such cell lines may then be used to infect a tissue cell line, such as NIH 3T3 cells, to produce large quantities of chimeric retroviral virions. Retroviral vectors may be administered by traditional methods (i.e., injection) or by implantation of a "producer cell line" in proximity to the target cell population (Culver, K., *et al.*, 1994, *Hum. Gene Ther.*, 5 (3): 343-79; Culver, K., *et al.*, *Cold Spring Harb. Symp. Quant. Biol.*, 59: 685-90); Oldfield, E., 1993, *Hum. Gene Ther.*, 4 (1): 39-69). The producer cell line is engineered to produce a viral vector and releases viral particles in the vicinity of the target cell. A portion of the released viral particles contact the target cells and infect those cells, thus delivering a nucleic acid of the present invention to the target cell. Following infection of the target cell, expression of the nucleic acid of the vector occurs.

Adenoviral vectors have proven especially useful for gene transfer into eukaryotic cells (Rosenfeld, M., *et al.*, 1991, *Science*, 252 (5004): 431-4; Crystal, R., *et al.*, 1994, *Nat. Genet.*, 8 (1): 42-51), the study eukaryotic gene expression (Levrero, M., *et al.*, 1991, *Gene*, 101 (2): 195-202), vaccine development (Graham, F. and Prevec, L., 1992, *Biotechnology*, 20: 363-90), and in animal models (Stratford-Perricaudet, L., *et al.*, 1992, *Bone Marrow Transplant.*, 9 (Suppl. 1): 151-2 ; Rich, D., *et al.*, 1993, *Hum. Gene Ther.*, 4 (4): 461-76). Experimental routes for administrating recombinant Ad to different tissues *in vivo* have included intratracheal instillation (Rosenfeld, M., *et al.*, 1992, *Cell*, 68 (1): 143-55) injection into muscle (Quantin, B., *et al.*, 1992, *Proc. Natl. Acad. Sci. U.S.A.*, 89 (7): 2581-4), peripheral intravenous injection (Herz, J., and Gerard, R., 1993, *Proc. Natl. Acad. Sci. U.S.A.*, 90 (7): 2812-6) and stereotactic inoculation to brain (Le Gal La Salle, G., *et al.*, 1993, *Science*, 259 (5097): 988-90), among others.

Adeno-associated virus (AAV) demonstrates high-level infectivity, broad host range and specificity in integrating into the host cell genome (Hermonat, P., et al., 1984, *Proc. Natl. Acad. Sci. U.S.A.*, 81 (20): 6466-70). And Herpes Simplex Virus type-1 (HSV-1) is yet another attractive vector system, especially for use in the nervous system because of its neurotropic property (Geller, A., *et al.*, 1991, *Trends Neurosci.*, 14 (10): 428-32; Glorioso, *et al.*, 1995, *Mol. Biotechnol.*, 4 (1): 87-99; Glorioso, *et al.*, 1995, *Annu. Rev. Microbiol.*, 49: 675-710).

Poxvirus is another useful expression vector (Smith, et al. 1983, *Gene*, 25 (1): 21-8; Moss, et al, 1992, *Biotechnology*, 20: 345-62; Moss, et al, 1992, *Curr. Top. Microbiol. Immunol.*, 158: 25-38; Moss, et al. 1991. *Science*, 252: 1662-1667). Poxviruses shown to be useful include vaccinia, NYVAC, avipox, fowlpox, canarypox, ALVAC, and ALVAC(2), among others.

NYVAC (vP866) was derived from the Copenhagen vaccine strain of vaccinia virus by deleting six nonessential regions of the genome encoding known or potential virulence factors (see, for example, U.S. Pat. Nos. 5,364,773 and 5,494,807). The deletion loci were also engineered as recipient loci for the insertion of foreign genes. The deleted regions are: thymidine kinase gene (TK; J2R); hemorrhagic region (u; B13R+B14R); A type inclusion body region (ATI; A26L); hemagglutinin gene (HA; A56R); host range gene region (C7L-K1L); and, large subunit, ribonucleotide reductase (I4L). NYVAC is a genetically engineered vaccinia virus strain that was generated by the specific deletion of eighteen open reading frames encoding gene products associated with virulence and host range. NYVAC has been show to be useful for expressing TAs (see, for example, U.S. Pat. No. 6,265,189). NYVAC (vP866), vP994, vCP205, vCP1433, placZH6H4Lreverse, pMPC6H6K3E3 and pC3H6FHVB were also deposited with the ATCC under the terms of the Budapest Treaty, accession numbers VR-2559, VR-2558, VR-2557, VR-2556, ATCC-97913, ATCC-97912, and ATCC-97914, respectively.

ALVAC-based recombinant viruses (i.e., ALVAC-1 and ALVAC-2) are also suitable for use in practicing the present invention (see, for example, U.S. Pat. No. 5,756,103). ALVAC(2) is identical to ALVAC(1) except that ALVAC(2) genome comprises the vaccinia E3L and K3L genes under the control of vaccinia promoters (U.S. Pat. No. 6,130,066; Beattie et al., 1995a, 1995b, 1991; Chang et al., 1992; Davies et al., 1993). Both ALVAC(1) and ALVAC(2) have been demonstrated to be useful in expressing foreign DNA sequences, such as TAs (Tartaglia et al., 1993 a,b; U.S. Pat. No. 5,833,975). ALVAC was deposited under the terms of the Budapest

Treaty with the American Type Culture Collection (ATCC), 10801 University Boulevard, Manassas, Va. 20110-2209, USA, ATCC accession number VR-2547.

Another useful poxvirus vector is TROVAC. TROVAC refers to an attenuated fowlpox that was a plaque-cloned isolate derived from the FP-1 vaccine strain of fowlpoxvirus which is licensed for vaccination of 1 day old chicks. TROVAC was likewise deposited under the terms of the Budapest Treaty with the ATCC, accession number 2553.

"Non-viral" plasmid vectors may also be suitable in practicing the present invention. Preferred plasmid vectors are compatible with bacterial, insect, and / or mammalian host cells. Such vectors include, for example, PCR-II, pCR3, and pcDNA3.1 (Invitrogen, San Diego, CA), pBSII (Stratagene, La Jolla, CA), pET15 (Novagen, Madison, WI), pGEX (Pharmacia Biotech, Piscataway, NJ), pEGFP-N2 (Clontech, Palo Alto, CA), pETL (BlueBacII, Invitrogen), pDSR-alpha (PCT pub. No. WO 90/14363) and pFastBacDual (Gibco-BRL, Grand Island, NY) as well as Bluescript® plasmid derivatives (a high copy number COLE1-based phagemid, Stratagene Cloning Systems, La Jolla, CA), PCR cloning plasmids designed for cloning Taq-amplified PCR products (*e.g.*, TOPO™ TA cloning® kit, PCR2.1® plasmid derivatives, Invitrogen, Carlsbad, CA). Bacterial vectors may also be used with the current invention. These vectors include, for example, *Shigella, Salmonella, Vibrio cholerae, Lactobacillus, Bacille calmette guérin (BCG), and Streptococcus* (see for example, WO 88/6626; WO 90/0594; WO 91/13157; WO 92/1796; and WO 92/21376). Many other non-viral plasmid expression vectors and systems are known in the art and could be used with the current invention.

Suitable nucleic acid delivery techniques include DNA-ligand complexes, adenovirus-ligand-DNA complexes, direct injection of DNA, $CaPO_4$ precipitation, gene gun techniques, electroporation, and colloidal dispersion systems, among others. Colloidal dispersion systems include macromolecule complexes, nanocapsules, microspheres, beads, and lipid-based systems including oil-in-water emulsions, micelles, mixed micelles, and liposomes. The preferred colloidal system of this invention is a liposome, which are artificial membrane vesicles useful as delivery vehicles *in vitro* and *in vivo*. RNA, DNA and intact virions can be encapsulated within the aqueous interior and be delivered to cells in a biologically active form (Fraley, R., *et al.*, 1981, *Trends Biochem. Sci.*, 6: 77). The composition of the liposome is usually a combination of phospholipids, particularly high-phase-transition-temperature phospholipids, usually in

combination with steroids, especially cholesterol. Other phospholipids or other lipids may also be used. The physical characteristics of liposomes depend on pH, ionic strength, and the presence of divalent cations. Examples of lipids useful in liposome production include phosphatidyl compounds, such as phosphatidylglycerol, phosphatidylcholine, phosphatidylserine, phosphatidylethanolamine, sphingolipids, cerebrosides, and gangliosides. Particularly useful are diacylphosphatidylglycerols, where the lipid moiety contains from 14-18 carbon atoms, particularly from 16-18 carbon atoms, and is saturated. Illustrative phospholipids include egg phosphatidylcholine, dipalmitoylphosphatidylcholine and distearoylphosphatidylcholine.

An immunogenic target may also be administered in combination with one or more adjuvants to boost the immune response. Exemplary adjuvants are shown in Table II below:

Table II

Types of Immunologic Adjuvants

Type of Adjuvant	General Examples	Specific Examples/References
Gel-type	Aluminum hydroxide/phosphate ("alum adjuvants")	(Aggerbeck and Heron, 1995)
	Calcium phosphate	(Relyveld, 1986)
Microbial	Muramyl dipeptide (MDP)	(Chedid et al., 1986)
	Bacterial exotoxins	Cholera toxin (CT), *E.coli* labile toxin (LT)(Freytag and Clements, 1999)
	Endotoxin-based adjuvants	Monophosphoryl lipid A (MPL) (Ulrich and Myers, 1995)
	Other bacterial	CpG oligonucleotides (Corral and Petray, 2000), BCG sequences (Krieg, et al. *Nature*, 374:576), tetanus toxoid (Rice, et al. *J. Immunol.*, 2001, 167: 1558-1565)
Particulate	Biodegradable Polymer microspheres	(Gupta et al., 1998)
	Immunostimulatory complexes (ISCOMs)	(Morein and Bengtsson, 1999)
	Liposomes	(Wassef et al., 1994)
Oil-emulsion and surfactant-based adjuvants	Freund's incomplete adjuvant	(Jensen et al., 1998)
	Microfluidized emulsions	MF59 (Ott et al., 1995)
		SAF (Allison and Byars, 1992) (Allison, 1999)
	Saponins	QS-21 (Kensil, 1996)
Synthetic	Muramyl peptide derivatives	Murabutide (Lederer, 1986) Threony-MDP (Allison, 1997)
	Nonionic block copolymers	L121 (Allison, 1999)
	Polyphosphazene (PCPP)	(Payne et al., 1995)

	Synthetic polynucleotides	Poly A:U, Poly I:C (Johnson, 1994)
	Thalidomide derivatives	CC-4047/ACTIMID (J. Immunol., 168(10):4914-9)

Administration of a composition of the present invention to a host may be accomplished using any of a variety of techniques known to those of skill in the art. The composition(s) may be processed in accordance with conventional methods of pharmacy to produce medicinal agents for administration to patients, including humans and other mammals (i.e., a "pharmaceutical composition"). The pharmaceutical composition is preferably made in the form of a dosage unit containing a given amount of DNA, viral vector particles, polypeptide or peptide, for example. A suitable daily dose for a human or other mammal may vary widely depending on the condition of the patient and other factors, but, once again, can be determined using routine methods.

The pharmaceutical composition may be administered orally, parentally, by inhalation spray, rectally, intranodally, or topically in dosage unit formulations containing conventional pharmaceutically acceptable carriers, adjuvants, and vehicles. The term "pharmaceutically acceptable carrier" or "physiologically acceptable carrier" as used herein refers to one or more formulation materials suitable for accomplishing or enhancing the delivery of a nucleic acid, polypeptide, or peptide as a pharmaceutical composition. A "pharmaceutical composition" is a composition comprising a therapeutically effective amount of a nucleic acid or polypeptide. The terms "effective amount" and "therapeutically effective amount" each refer to the amount of a nucleic acid or polypeptide used to induce or enhance an effective immune response. It is preferred that compositions of the present invention provide for the induction or enhancement of an anti-tumor immune response in a host which protects the host from the development of a tumor and / or allows the host to eliminate an existing tumor from the body.

For oral administration, the pharmaceutical composition may be of any of several forms including, for example, a capsule, a tablet, a suspension, or liquid, among others. Liquids may be administered by injection as a composition with suitable carriers including saline, dextrose, or water. The term parenteral as used herein includes subcutaneous, intravenous, intramuscular, intrasternal, infusion, or intraperitoneal administration. Suppositories for rectal administration of the drug can be prepared by mixing the drug with a suitable non-irritating excipient such as cocoa butter and polyethylene glycols that are solid at ordinary temperatures but liquid at the rectal temperature.

The dosage regimen for immunizing a host or otherwise treating a disorder or a disease with a composition of this invention is based on a variety of factors, including the type of disease, the age, weight, sex, medical condition of the patient, the severity of the condition, the route of administration, and the particular compound employed. For example, a poxviral vector may be administered as a composition comprising 1 x 10^6 infectious particles per dose. Thus, the dosage regimen may vary widely, but can be determined routinely using standard methods.

A prime-boost regimen may also be utilized (WO 01/30382 A1) in which the targeted immunogen is initially administered in a priming step in one form followed by a boosting step in which the targeted immunogen is administered in another form. The form of the targeted immunogen in the priming and boosting steps are different. For instance, if the priming step utilized a nucleic acid, the boost may be administered as a peptide. Similarly, where a priming step utilized one type of recombinant virus (i.e., ALVAC), the boost step may utilize another type of virus (i.e., NYVAC). This prime-boost method of administration has been shown to induce strong immunological responses. Various combinations of forms are suitable in practicing the present invention.

While the compositions of the invention can be administered as the sole active pharmaceutical agent, they can also be used in combination with one or more other compositions or agents (i.e., other immunogenic targets, co-stimulatory molecules, adjuvants). When administered as a combination, the individual components can be formulated as separate compositions administered at the same time or different times, or the components can be combined as a single composition.

Injectable preparations, such as sterile injectable aqueous or oleaginous suspensions, may be formulated according to known methods using suitable dispersing or wetting agents and suspending agents. The injectable preparation may also be a sterile injectable solution or suspension in a non-toxic parenterally acceptable diluent or solvent. Suitable vehicles and solvents that may be employed are water, Ringer's solution, and isotonic sodium chloride solution, among others. For instance, a viral vector such as a poxvirus may be prepared in 0.4% NaCl. In addition, sterile, fixed oils are conventionally employed as a solvent or suspending medium. For this purpose, any bland fixed oil may be employed, including synthetic mono- or diglycerides. In addition, fatty acids such as oleic acid find use in the preparation of injectables.

For topical administration, a suitable topical dose of a composition may be administered one to four, and preferably two or three times daily. The dose may also be administered with intervening days during which no does is applied. Suitable compositions may comprise from 0.001% to 10% w/w, for example, from 1% to 2% by weight of the formulation, although it may comprise as much as 10% w/w, but preferably not more than 5% w/w, and more preferably from 0.1% to 1% of the formulation. Formulations suitable for topical administration include liquid or semi-liquid preparations suitable for penetration through the skin (*e.g.*, liniments, lotions, ointments, creams, or pastes) and drops suitable for administration to the eye, ear, or nose.

The pharmaceutical compositions may also be prepared in a solid form (including granules, powders or suppositories). The pharmaceutical compositions may be subjected to conventional pharmaceutical operations such as sterilization and/or may contain conventional adjuvants, such as preservatives, stabilizers, wetting agents, emulsifiers, buffers etc. Solid dosage forms for oral administration may include capsules, tablets, pills, powders, and granules. In such solid dosage forms, the active compound may be admixed with at least one inert diluent such as sucrose, lactose, or starch. Such dosage forms may also comprise, as in normal practice, additional substances other than inert diluents, *e.g.*, lubricating agents such as magnesium stearate. In the case of capsules, tablets, and pills, the dosage forms may also comprise buffering agents. Tablets and pills can additionally be prepared with enteric coatings. Liquid dosage forms for oral administration may include pharmaceutically acceptable emulsions, solutions, suspensions, syrups, and elixirs containing inert diluents commonly used in the art, such as water. Such compositions may also comprise adjuvants, such as wetting sweetening, flavoring, and perfuming agents.

Pharmaceutical compositions comprising a nucleic acid or polypeptide of the present invention may take any of several forms and may be administered by any of several routes. In preferred embodiments, the compositions are administered via a parenteral route (intradermal, intramuscular or subcutaneous) to induce an immune response in the host. Alternatively, the composition may be administered directly into a lymph node (intranodal) or tumor mass (i.e., intratumoral administration). For example, the dose could be administered subcutaneously at days 0, 7, and 14. Suitable methods for immunization using compositions comprising TAs are known in the art, as shown for p53 (Hollstein et al., 1991), p21-ras (Almoguera et al., 1988), HER-2 (Fendly et al., 1990), the melanoma-associated antigens (MAGE-1; MAGE-2) (van der

Bruggen et al., 1991), p97 (Hu et al., 1988), melanoma-associated antigen E (WO 99/30737) and carcinoembryonic antigen (CEA) (Kantor et al., 1993; Fishbein et al., 1992; Kaufman et al., 1991), among others.

Preferred embodiments of administratable compositions include, for example, nucleic acids or polypeptides in liquid preparations such as suspensions, syrups, or elixirs. Preferred injectable preparations include, for example, nucleic acids or polypeptides suitable for parental, subcutaneous, intradermal, intramuscular or intravenous administration such as sterile suspensions or emulsions. For example, a recombinant poxvirus may be in admixture with a suitable carrier, diluent, or excipient such as sterile water, physiological saline, glucose or the like. The composition may also be provided in lyophilized form for reconstituting, for instance, in isotonic aqueous, saline buffer. In addition, the compositions can be co-administered or sequentially administered with other antineoplastic, anti-tumor or anti-cancer agents and/or with agents which reduce or alleviate ill effects of antineoplastic, anti-tumor or anti-cancer agents.

A kit comprising a composition of the present invention is also provided. The kit can include a separate container containing a suitable carrier, diluent or excipient. The kit can also include an additional anti-cancer, anti-tumor or antineoplastic agent and/or an agent that reduces or alleviates ill effects of antineoplastic, anti-tumor or anti-cancer agents for co- or sequential-administration. Additionally, the kit can include instructions for mixing or combining ingredients and/or administration.

A better understanding of the present invention and of its many advantages will be had from the following examples, given by way of illustration.

EXAMPLES

Example 1

Construction of the Multi-Antigen Construct vT416

The expression vector vT416 (ALVAC-NY-ESO-1/Trp-2-LFA-3/ICAM-1/B7.1-E3L/K3L) was constructed in the ALVAC vector using standard techniques. DNA sequences encoding NY-ESO-1, Trp-2, LFA-3, ICAM-1, B7.1, vvE3L and vvK3L were inserted into various loci within the ALVAC genome. DNA sequences encoding NY-ESO-1 (Chen et al. 1997 PNAS 94:1914) and TRP-2 (Wang et al. 1996 J. Exp. Med. 184:2207) were inserted into

the C5 locus. DNA sequences encoding LFA-3 (Wallner, et al. (1987) J. Exp. Med. 166:923-932), ICAM-1 (Staunton, et al. (1988) Cell 52:925-933) and B7.1 (Chen, et al. (1992) Cell 71:1093-1102) were inserted into the C3 locus. LFA-3, ICAM-1 and B7.1 form an expression cassette known as TRICOM. DNA sequences encoding vvE3L (Chang, et al. 1992. Proc. Natl. Acad. Sci. U. S. A 89:4825-4829) and vvK3L (Beattie, et al. 1991. Virology 183:419-422) were inserted into the C6 locus. Promoters were utilized as follows:

Table III

DNA sequence	Promoter
E3L	vaccinia E3L
K3L	vaccinia H6
LFA-3	vaccinia 30K
ICAM-1	vaccinia I3
B7.1	sE/L
NY-ESO-1	vaccinia H6
TRP-2	sE/L

Promoter sE/L is described by Chakrabarti, et al. (BioTechniques 23: 1094-1097, 1997).

The donor plasmids utilized are shown below:

Table IV

Plasmid	Size (bp)	Vector	Antibiotic Resitance Gene
pMPC6H6K3E3	-	pBS-SK	Amp
pALVAC.Tricom(C3) #33	10,470	pBS-SK	Amp
pT1132	11,154	pBS-SK	Amp

NY-ESO-1 and TRP-2 DNA sequences were inserted into the ALVAC donor plasmid pT1132. This donor plasmid was then used with pALVAC.Tricom(C3) #33 to generate the ALVAC-TRICOM recombinant expressing these genes using standard techniques. The plasmids pALVAC.Tricom(C3) #33 and pT1132 are shown in **Figure 1.** The DNA sequences of pALVAC.Tricom(C3) #33 and pT1132 are shown in **Figures 2** and **3**, respectively.

Example 2

Construction of the Multi-Antigen Construct vT419

The expression vector vT419 (ALVAC-gp100M/Mart-1/ Mage-1,3 minigene-LFA-3/ICAM-1/B7.1-E3L/K3L) was constructed in the ALVAC vector using standard techniques. DNA sequences encoding the gp100M/MART-1/MAGE-1,3 minigene, LFA-3, ICAM-1, B7.1, vvE3L and vvK3L were inserted into various loci within the ALVAC genome. The gp100M/ MART-1/MAGE-1,3 minigene was inserted into the C5 locus. DNA sequences encoding LFA-3 (Wallner, et al. (1987) J. Exp. Med. 166:923-932), ICAM-1 (Staunton, et al. (1988) Cell 52:925-933) and B7.1 (Chen, et al. (1992) Cell 71:1093-1102) were inserted into the C3 locus. LFA-3, ICAM-1 and B7.1 form an expression cassette known as TRICOM. DNA sequences encoding vvE3L (Chang, et al. 1992. Proc. Natl. Acad. Sci. U. S. A 89:4825-4829) and vvK3L (Beattie, et al. 1991. Virology 183:419-422) were inserted into the C6 locus. Promoters were utilized as follows:

Table V

Gene	Promoter
E3L	vaccinia E3L
K3L	vaccinia H6
LFA-3	vaccinia 30K
ICAM-1	vaccinia I3
B7.1	sE/L
gp100(M)	vaccinia H6
Mart-1	vaccinia 42K

Promoter sE/L is described by Chakrabarti, et al. (BioTechniques 23: 1094-1097, 1997).

The donor plasmids utilized are shown below:

Table VI

Plasmid	Size (bp)	Vector	Antibiotic Resitance Gene
PMPC6H6K3E3	-	pBS-SK	Amp
pALVAC.Tricom(C3) #33	10,470	pBS-SK	Amp
pT3217	11,465	pBS-SK	Amp

gp100(M), Mart-1 and Mage-1,3 minigene were inserted into the ALVAC C5 donor plasmid pT3217. This donor plasmid was then used with pALVAC.Tricom(C3) #33 to generate the ALVAC-TRICOM recombinant expressing these genes using standard techniques. This donor plasmid inserts into the C5 site. pALVAC.Tricom(C3) #33 is shown in **Figures 1** and **2.** The pT3217 plasmid is shown in **Figure 4.** The DNA sequence of pT3217 is shown in **Figure 5.**

EXAMPLE 3

Immunological Assessment of Multi-Antigen Vectors

The results of the first animal experiment indicated a trend toward higher immunological responses to three (Mart 1, NY-ESO-1 and gp100) of the four antigens when the vaccine was given as two separate injections. However, these differences were not statistically significant. In detail, HLA-A2/K^b transgenic mice (5/group) were immunized subcutaneously with vT419 (ALVAC(2)-gp100M/MART-1/MAGE-1/3 minigene/TRICOM) and vT416 (ALVAC(2)-TRP-2/NY-ESO-1/TRICOM) either combined at one site or given as separate injections. Control mice were immunized with parental ALVAC(2). Mice were vaccinated three times (at three week intervals), and three weeks after the last boost T cell responses in individual mice were analyzed by IFN-g ELISPOT and CTL assays following in vitro restimulation with peptide. Compared to control animals, mice vaccinated with the multi-antigen vectors (at 2 sites) exhibited statistically significant ELISPOT responses against MART-1. The IFN-gamma response to gp100M and NY-ESO-1 were also detectable, although these responses were not statistically significant due to response variability and the small number of cultures tested. ELISPOT responses against the TRP-2 antigen were elevated in all groups tested (including control animals), presumably due to the fact that the dominant A2-restricted TRP-2 peptide (180-188) cross-reacts with H-$2K^b$ and can induce low avidity T cell responses in naïve mice following in vitro culture, and were therefore not statistically significant. Interestingly, ELISPOT responses in mice injected with an admixture of vT416 and vT419 were generally lower than in mice receiving each virus separately, although these differences did not achieve statistical significance. The CTL data were largely negative, except for one strong anti-gp100 response and one marginal anti-MART-1 response, both of which occurred in mice vaccinated with vT416 and vT419 (two sites). Overall, these results provided encouraging data that establish that the multi-antigen vectors can generate

responses against MART-1, and suggest that anti-gp100 and anti-NY-ESO-1 responses can also be induced.

Two additional pre-clinical animal studies have been completed using the melanoma multi-antigen ALVAC recombinants. In these experiments, HLA-A2/K^b transgenic mice (5/group) were immunized subcutaneously with vT419 (ALVAC(2)-gp100M/MART-1/MAGE-1/3 minigene/TRICOM) and vT416 (ALVAC(2)-TRP-2/NY-ESO-1/TRICOM) either combined at one site or given as separate injections. Control mice were immunized with parental ALVAC(2). After vaccination, the T cell responses in individual mice were assessed by IFN-gamma ELISPOT assay following in vitro restimulation with peptide. Unlike the previous multi-antigen experiment, which provided encouraging immunogenicity data, the two most recent studies generated inconclusive data, due to high background responses in control immunized animals. Therefore, overall the results were deemed as inconclusive.

To confirm the immunogenicity of the multi-antigen constructs, and to repeat results from the first study, another pre-clinical animal study has been completed. HLA-A2/K^b transgenic mice (10/group) were immunized subcutaneously with vT419 (ALVAC(2)-gp100M/MART-1/MAGE-1/3 minigene/TRICOM) and vT416 (ALVAC(2)-TRP-2/NY-ESO-1/TRICOM) given as separate injections. Control mice were immunized with parental ALVAC(2). Statistically significant ELISPOT responses were detectable against gp100, Mart-1 and TRP-2, and some responses were detected against NY-ESO-1, which were at the border of being statistically significant.

While the present invention has been described in terms of the preferred embodiments, it is understood that variations and modifications will occur to those skilled in the art. Therefore, it is intended that the appended claims cover all such equivalent variations that come within the scope of the invention as claimed.

CLAIMS

What is claimed is:

1. An expression vector for co-expressing at least two immunogenic targets, wherein said immunogenic targets are selected from the group consisting of NY-ESO-1, TRP-2, gp100, gp100M, a MART antigen, MART-1, a MAGE antigen, MAGE-1, and MAGE-3.
2. The expression vector of claim 1 wherein the vector is a plasmid or a viral vector.
3. The expression vector of claim 2 wherein the viral vector is selected from the group consisting of poxvirus, adenovirus, retrovirus, herpesvirus, and adeno-associated virus.
4. The expression vector of claim 3 wherein the viral vector is a poxvirus selected from the group consisting of vaccinia, NYVAC, avipox, canarypox, ALVAC, ALVAC(2), fowlpox, and TROVAC.
5. The expression vector of claim 4 wherein the viral vector is a poxvirus selected from the group consisting of NYVAC, ALVAC, and ALVAC(2).
6. The expression vector of claim 1 further comprising at least one nucleic sequence encoding an angiogenesis-associated antigen.
7. The expression vector of claim 6 wherein the vector is a plasmid or a viral vector.
8. The expression vector of claim 7 wherein the viral vector is selected from the group consisting of poxvirus, adenovirus, retrovirus, herpesvirus, and adeno-associated virus.
9. The expression vector of claim 8 wherein the viral vector is a poxvirus selected from the group consisting of vaccinia, NYVAC, avipox, canarypox, ALVAC, ALVAC(2), fowlpox, and TROVAC.
10. The expression vector of claim 9 wherein the viral vector is a poxvirus selected from the group consisting of NYVAC, ALVAC, and ALVAC(2).
11. The expression vector of claim 1 or 6 further comprising at least one nucleic acid sequence encoding a co-stimulatory component.
12. The expression vector of claim 11 wherein the vector is a plasmid or a viral vector.
13. The expression vector of claim 12 wherein the viral vector is selected from the group consisting of poxvirus, adenovirus, retrovirus, herpesvirus, and adeno-associated virus.
14. The expression vector of claim 13 wherein the viral vector is a poxvirus selected from the group consisting of vaccinia, NYVAC, avipox, canarypox, ALVAC, ALVAC(2), fowlpox, and TROVAC.

15. The expression vector of claim 14 wherein the viral vector is a poxvirus selected from the group consisting of NYVAC, ALVAC, and ALVAC(2).

16. The expression vector of any one claims 11-15 wherein the co-stimulatory component is human B7.1.

17. A composition comprising an expression vector of any one of claims 1-16 in a pharmaceutically acceptable carrier.

18. A method for preventing or treating cancer comprising administering to a host an expression vector of any one of claims 1-16.

19. A method for preventing or treating cancer comprising administering to a host a composition of claim 17.

FIGURE 1

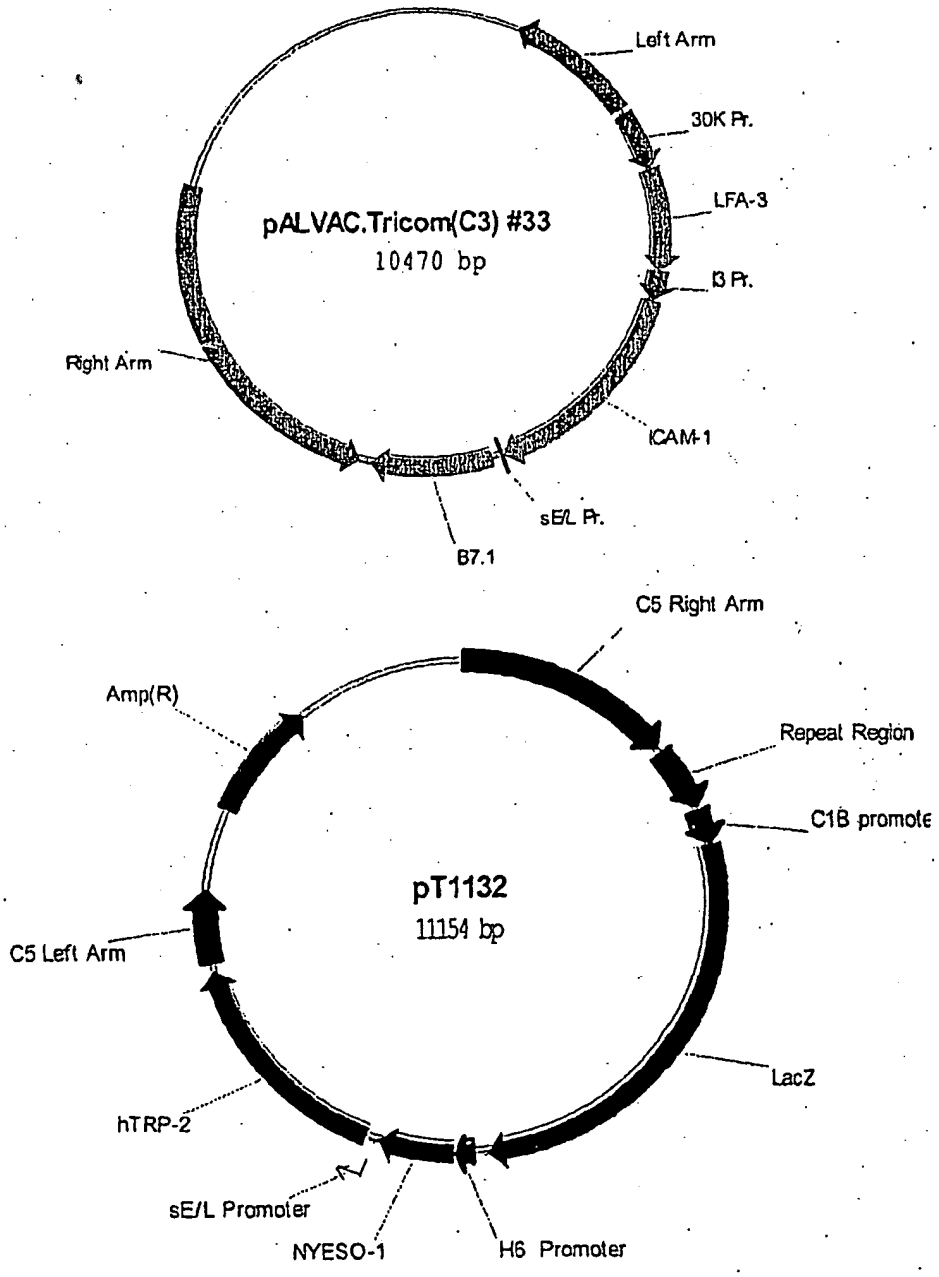

FIGURE 2

DNA Sequence of pALVAC.Tricom(C3) #33

```
       1  GGAAATTGTA AACGTTAATA TTTTGTTAAA ATTCGCGTTA AATTTTTGTT
          CCTTTAACAT TTGCAATTAT AAAACAATTT TAAGCGCAAT TTAAAAACAA
      51  AAATCAGCTC ATTTTTTAAC CAATAGGCCG AAATCGGCAA AATCCCTTAT
          TTTAGTCGAG TAAAAAATTG GTTATCCGGC TTTAGCCGTT TTAGGGAATA
     101  AAATCAAAAG AATAGACCGA GATAGGGTTG AGTGTTGTTC CAGTTTGGAA
          TTTAGTTTTC TTATCTGGCT CTATCCCAAC TCACAACAAG GTCAAACCTT
     151  CAAGAGTCCA CTATTAAAGA ACGTGGACTC CAACGTCAAA GGGCGAAAAA
          GTTCTCAGGT GATAATTTCT TGCACCTGAG GTTGCAGTTT CCCGCTTTTT
     201  CCGTCTATCA GGGCGATGGC CCACTACGTG AACCATCACC CTAATCAAGT
          GGCAGATAGT CCCGCTACCG GGTGATGCAC TTGGTAGTGG GATTAGTTCA
     251  TTTTTGGGGT CGAGGTGCCG TAAAGCACTA AATCGGAACC CTAAAGGGAG
          AAAAACCCCA GCTCCACGGC ATTTCGTGAT TTAGCCTTGG GATTTCCCTC
     301  CCCCCGATTT AGAGCTTGAC GGGGAAAGCC GGCGAACGTG GCGAGAAAGG
          GGGGGCTAAA TCTCGAACTG CCCCTTTCGG CCGCTTGCAC CGCTCTTTCC
     351  AAGGGAAGAA AGCGAAAGGA GCGGGCGCTA GGGCGCTGGC AAGTGTAGCG
          TTCCCTTCTT TCGCTTTCCT CGCCCGCGAT CCCGCGACCG TTCACATCGC
     401  GTCACGCTGC GCGTAACCAC CACACCCGCC GCGCTTAATG CGCCGCTACA
          CAGTGCGACG CGCATTGGTG GTGTGGGCGG CGCGAATTAC GCGGCGATGT
     451  GGGCGCGTCG CGCCATTCGC CATTCAGGCT GCGCAACTGT TGGGAAGGGC
          CCCGCGCAGC GCGGTAAGCG GTAAGTCCGA CGCGTTGACA ACCCTTCCCG
     501  GATCGGTGCG GGCCTCTTCG CTATTACGCC AGCTGGCGAA AGGGGGATGT
          CTAGCCACGC CCGGAGAAGC GATAATGCGG TCGACCGCTT TCCCCCTACA
     551  GCTGCAAGGC GATTAAGTTG GGTAACGCCA GGGTTTTCCC AGTCACGACG
          CGACGTTCCG CTAATTCAAC CCATTGCGGT CCCAAAAGGG TCAGTGCTGC
     601  TTGTAAAACG ACGGCCAGTG AATTGTAATA CGACTCACTA TAGGGCGAAT
          AACATTTTGC TGCCGGTCAC TTAACATTAT GCTGAGTGAT ATCCCGCTTA
     651  TGGGTACCGC GGCCGCGTCG ACATGCATTG TTAGTTCTGT AGATCAGTAA
          ACCCATGGCG CCGGCGCAGC TGTACGTAAC AATCAAGACA TCTAGTCATT
               ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
                                  Left Arm
     701  CGTATAGCAT ACGAGTATAA TTATCGTAGG TAGTAGGTAT CCTAAAATAA
          GCATATCGTA TGCTCATATT AATAGCATCC ATCATCCATA GGATTTTATT
          ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
                                  Left Arm
     751  ATCTGATACA GATAATAACT TTGTAAATCA ATTCAGCAAT TTCTCTATTA
          TAGACTATGT CTATTATTGA AACATTTAGT TAAGTCGTTA AAGAGATAAT
          ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
                                  Left Arm
     801  TCATGATAAT GATTAATACA CAGCGTGTCG TTATTTTTTG TTACGATAGT
          AGTACTATTA CTAATTATGT GTCGCACAGC AATAAAAAAC AATGCTATCA
          ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
                                  Left Arm
     851  ATTTCTAAAG TAAAGAGCAG GAATCCCTAG TATAATAGAA ATAATCCATA
          TAAAGATTTC ATTTCTCGTC CTTAGGGATC ATATTATCTT TATTAGGTAT
          ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
                                  Left Arm
     901  TGAAAAATAT AGTAATGTAC ATATTTCTAA TGTTAACATA TTTATAGGTA
          ACTTTTTATA TCATTACATG TATAAAGATT ACAATTGTAT AAATATCCAT
          ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
                                  Left Arm
     951  AATCCAGGAA GGGTAATTTT TACATATCTA TATACGCTTA TTACAGTTAT
          TTAGGTCCTT CCCATTAAAA ATGTATAGAT ATATGCGAAT AATGTCAATA
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                ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
                                    Left Arm
      1001      TAAAAATATA CTTGCAAACA TGTTAGAAGT AAAAAAGAAA GAACTAATTT
                ATTTTTATAT GAACGTTTGT ACAATCTTCA TTTTTTCTTT CTTGATTAAA
                ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
                                    Left Arm
      1051      TACAAAGTGC TTTACCAAAA TGCCAATGGA AATTACTTAG TATGTATATA
                ATGTTTCACG AAATGGTTTT ACGGTTACCT TTAATGAATC ATACATATAT
                ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
                                    Left Arm
      1101      ATGTATAAAG GTATGAATAT CACAAACAGC AAATCGGCTA TTCCCAAGTT
                TACATATTTC CATACTTATA GTGTTTGTCG TTTAGCCGAT AAGGGTTCAA
                ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
                                    Left Arm

      1151      GAGAAACGGT ATAATAGATA TATTTCTAGA TACCATTAAT AACCTTATAA
                CTCTTTGCCA TATTATCTAT ATAAAGATCT ATGGTAATTA TTGGAATATT
                ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
                                    Left Arm
      1201      GCTTGACGTT TCCTATAATG CCTACTAAGA AAACTAGAAG ATACATACAT
                CGAACTGCAA AGGATATTAC GGATGATTCT TTTGATCTTC TATGTATGTA
                ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
                                    Left Arm
      1251      ACTAACGCCA TACGAGAGTA ACTACTCATC GTATAACTAC TGTTGCTAAC
                TGATTGCGGT ATGCTCTCAT TGATGAGTAG CATATTGATG ACAACGATTG
                ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
                                    Left Arm
      1301      AGTGACACTG ATGTTATAAC TCATCTTTGA TGTGGTATAA ATGTATAATA
                TCACTGTGAC TACAATATTG AGTAGAAACT ACACCATATT TACATATTAT
                ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
                                    Left Arm
      1351      ACTATATTAC ACTGGTATTT TATTTCAGTT ATATACTATA TAGTATTAAA
                TGATATAATG TGACCATAAA ATAAAGTCAA TATATGATAT ATCATAATTT
                ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
                                    Left Arm
      1401      AATTATATTT GTATAATTAT ATTATTATAT TCAGTGTAGA AAGTAAAATA
                TTAATATAAA CATATTAATA TAATAATATA AGTCACATCT TTCATTTTAT
                ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
                                    Left Arm
      1451      CTATAAATAT GTATCTCTTA TTTATAACTT ATTAGTAAAG TATGTACTAT
                GATATTTATA CATAGAGAAT AAATATTGAA TAATCATTTC ATACATGATA
                ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
                                    Left Arm
      1501      TCAGTTATAT TGTTTTATAA AAGCTAAATG CTACTAGATT GATATAAATG
                AGTCAATATA ACAAAATATT TTCGATTTAC GATGATCTAA CTATATTTAC
                ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
                                    Left Arm
      1551      AATATGTAAT AAATTAGTAA TGTAGTATAC TAATATTAAC TCACATTTGA
                TTATACATTA TTTAATCATT ACATCATATG ATTATAATTG AGTGTAAACT
                ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
                                    Left Arm
                                                                    30K Pr.
                                                                    ~~~~
      1601      CTAATTAGCT ATAAAAACCC TAAGGTAGGC GGCCGCACTA GAGGATTCGA
                GATTAATCGA TATTTTTGGG ATTCCATCCG CCGGCGTGAT CTCCTAAGCT
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                                30K Pr.
                    ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
          1651      CAAACACCAA TAATTCCCTT CTCTTCATTC CGGACATTAA ATTGGCTATA
                    GTTTGTGGTT ATTAAGGGAA GAGAAGTAAG GCCTGTAATT TAACCGATAT
                                30K Pr.
                    ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
          1701      GATAATAAAG ACATTGAGAT GTTACAGGCT CTGTTCAAAT ACGACATTAA
                    CTATTATTTC TGTAACTCTA CAATGTCCGA GACAAGTTTA TGCTGTAATT
                                30K Pr.
                    ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
          1751      TATCTATTCT GCTAATCTGG AAAATGTACT ATTGGATGAT GCCGAAATAG
                    ATAGATAAGA CGATTAGACC TTTTACATGA TAACCTACTA CGGCTTTATC
                                30K Pr.
                    ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
          1801      CTAAAATGAT TATAGAAAAG CATGTTGAAT ACAAGTCTGA CTCCTATACA
                    GATTTTACTA ATATCTTTTC GTACAACTTA TGTTCAGACT GAGGATATGT
                                30K Pr.
                    ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
          1851      AAAGATCTCG ATATAGTCAA GAATAATAAA TTGGATGAAA TAATTAGCAA
                    TTTCTAGAGC TATATCAGTT CTTATTATTT AACCTACTTT ATTAATCGTT
                                30K Pr.
                    ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
          1901      AAACAAGGAA CTCAGACTCA TGTACGTCAA TTGTGTAAAG AAAAACTAAT
                    TTTGTTCCTT GAGTCTGAGT ACATGCAGTT AACACATTTC TTTTTGATTA
                                30K Pr.
                    ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
          1951      TAGATTCTCC CACATTTTTG TTAACATTAC ACTAACTAAT TGGTAAAATT
                    ATCTAAGAGG GTGTAAAAAC AATTGTAATG TGATTGATTA ACCATTTTAA
                                30K Pr.
                    ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
          2001      GATAGAATAA TTATGTGTAT ATAAGATAGA TTTCCTATTG TCTTACTCAT
                    CTATCTTATT AATACACATA TATTCTATCT AAAGGATAAC AGAATGAGTA
                                30K Pr.
                    ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
                                                                hLFA-3
                                                    ~~~~~~~~~~~~~~~~~~~~
          2051      TGCATCGTGG GAATTCAGAT CAGCTTCCGC GGCATGGTTG CTGGGAGCGA
                    ACGTAGCACC CTTAAGTCTA GTCGAAGGCG CCGTACCAAC GACCCTCGCT
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                        hLFA-3
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2101    CGCGGGGCGG GCCCTGGGGG TCCTCAGCGT GGTCTGCCTG CTGCACTGCT
        GCGCCCCGCC CGGGACCCCC AGGAGTCGCA CCAGACGGAC GACGTGACGA
                        hLFA-3
        ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
2151    TTGGTTTCAT CAGCTGTTTT TCCCAACAAA TATATGGTGT TGTGTATGGG
        AACCAAAGTA GTCGACAAAA AGGGTTGTTT ATATACCACA ACACATACCC
                        hLFA-3
        ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
2201    AATGTAACTT TCCATGTACC AAGCAATGTG CCTTTAAAAG AGGTCCTATG
        TTACATTGAA AGGTACATGG TTCGTTACAC GGAAATTTTC TCCAGGATAC
                        hLFA-3
        ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
2251    GAAAAAACAA AAGGATAAAG TTGCAGAACT GGAAAATTCT GAATTCAGAG
        CTTTTTTGTT TTCCTATTTC AACGTCTTGA CCTTTTAAGA CTTAAGTCTC
                        hLFA-3
        ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
2301    CTTTCTCATC TTTTAAAAAT AGGGTTTATT TAGACACTGT GTCAGGTAGC
        GAAAGAGTAG AAAATTTTTA TCCCAAATAA ATCTGTGACA CAGTCCATCG
                        hLFA-3
        ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
2351    CTCACTATCT ACAACTTAAC ATCATCAGAT GAAGATGAGT ATGAAATGGA
        GAGTGATAGA TGTTGAATTG TAGTAGTCTA CTTCTACTCA TACTTTACCT
                        hLFA-3
        ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
2401    ATCGCCAAAT ATTACTGATA CCATGAAGTT CTTTCTTTAT GTGCTTGAGT
        TAGCGGTTTA TAATGACTAT GGTACTTCAA GAAAGAAATA CACGAACTCA
                        hLFA-3
        ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
2451    CTCTTCCATC TCCCACACTA ACTTGTGCAT TGACTAATGG AAGCATTGAA
        GAGAAGGTAG AGGGTGTGAT TGAACACGTA ACTGATTACC TTCGTAACTT
                        hLFA-3
        ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
2501    GTCCAATGCA TGATACCAGA GCATTACAAC AGCCATCGAG GACTTATAAT
        CAGGTTACGT ACTATGGTCT CGTAATGTTG TCGGTAGCTC CTGAATATTA
                        hLFA-3
        ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
2551    GTACTCATGG GATTGTCCTA TGGAGCAATG TAAACGTAAC TCAACCAGTA
        CATGAGTACC CTAACAGGAT ACCTCGTTAC ATTTGCATTG AGTTGGTCAT
                        hLFA-3
        ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
2601    TATATTTTAA GATGGAAAAT GATCTTCCAC AAAAAATACA GTGTACTCTT
        ATATAAAATT CTACCTTTTA CTAGAAGGTG TTTTTTATGT CACATGAGAA
                        hLFA-3
        ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
2651    AGCAATCCAT TATTTAATAC AACATCATCA ATCATTTTGA CAACCTGTAT
        TCGTTAGGTA ATAAATTATG TTGTAGTAGT TAGTAAAACT GTTGGACATA
                        hLFA-3
        ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
2701    CCCAAGCAGC GGTCATTCAA GACACAGATA TGCACTTATA CCCATACCAT
        GGGTTCGTCG CCAGTAAGTT CTGTGTCTAT ACGTGAATAT GGGTATGGTA
                        hLFA-3
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2751    TAGCAGTAAT TACAACATGT ATTGTGCTGT ATATGAATGG TATTCTGAAA
        ATCGTCATTA ATGTTGTACA TAACACGACA TATACTTACC ATAAGACTTT
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                         hLFA-3                                I3 Pr.
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2801      TGTGACAGAA AACCAGACAG AACCAACTCC AATTGATTGG CTCGACCGGG
          ACACTGTCTT TTGGTCTGTC TTGGTTGAGG TTAACTAACC GAGCTGGCCC
                                    I3 Pr.
          ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
2851      AATGTACTAT CTACGTACGA AACCCGCATC CGCTCCCATT CAATTCACAT
          TTACATGATA GATGCATGCT TTGGGCGTAG GCGAGGGTAA GTTAAGTGTA
                                    I3 Pr.
          ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
2901      TGGACAAGGA TAAAATAAAA CCACTGGTGG TTTGCGATTC CGAAATCTGT
          ACCTGTTCCT ATTTTATTTT GGTGACCACC AAACGCTAAG GCTTTAGACA
                                    I3 Pr.
          ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
2951      ACATCATGCA GTGGTTAAAC AAAAACATTT TTATTCTCAA ATGAGATAAA
          TGTAGTACGT CACCAATTTG TTTTTGTAAA AATAAGAGTT TACTCTATTT
                                    I3 Pr.
          ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
3001      GTGAAAATAT ATATCATTAT ATTACAAAGT ACAATTATTT AGGTTTAATC
          CACTTTTATA TATAGTAATA TAATGTTTCA TGTTAATAAA TCCAAATTAG
            I3 Pr.                                  hICAM
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3051      AATCCCGCGG GCTATGGCTC CCAGCAGCCC CCGGCCCGCG CTGCCCGCAC
          TTAGGGCGCC CGATACCGAG GGTCGTCGGG GGCCGGGCGC GACGGGCGTG
                                    hICAM
          ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
3101      TCCTGGTCCT GCTCGGGGCT CTGTTCCCAG GACCTGGCAA TGCCCAGACA
          AGGACCAGGA CGAGCCCCGA GACAAGGGTC CTGGACCGTT ACGGGTCTGT
                                    hICAM
          ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
3151      TCTGTGTCCC CCTCAAAAGT CATCCTGCCC CGGGGAGGCT CCGTGCTGGT
          AGACACAGGG GGAGTTTTCA GTAGGACGGG GCCCCTCCGA GGCACGACCA
                                    hICAM
          ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
3201      GACATGCAGC ACCTCCTGTG ACCAGCCCAA GTTGTTGGGC ATAGAGACCC
          CTGTACGTCG TGGAGGACAC TGGTCGGGTT CAACAACCCG TATCTCTGGG
                                    hICAM
          ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
3251      CGTTGCCTAA AAAGGAGTTG CTCCTGCCTG GGAACAACCG GAAGGTGTAT
          GCAACGGATT TTTCCTCAAC GAGGACGGAC CCTTGTTGGC CTTCCACATA
                                    hICAM
          ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
3301      GAACTGAGCA ATGTGCAAGA AGATAGCCAA CCAATGTGCT ATTCAAACTG
          CTTGACTCGT TACACGTTCT TCTATCGGTT GGTTACACGA TAAGTTTGAC
                                    hICAM
          ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
3351      CCCTGATGGG CAGTCAACAG CTAAAACCTT CCTCACCGTG TACTGGACTC
          GGGACTACCC GTCAGTTGTC GATTTTGGAA GGAGTGGCAC ATGACCTGAG
                                    hICAM
          ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
3401      CAGAACGGGT GGAACTGGCA CCCCTCCCCT CTTGGCAGCC AGTGGGCAAG
          GTCTTGCCCA CCTTGACCGT GGGGAGGGGA GAACCGTCGG TCACCCGTTC
                                    hICAM
          ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
3451      AACCTTACCC TACGCTGCCA GGTGGAGGGT GGGGCACCCC GGGCCAACCT
          TTGGAATGGG ATGCGACGGT CCACCTCCCA CCCCGTGGGG CCCGGTTGGA
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                          hICAM
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    3501  CACCGTGGTG CTGCTCCGTG GGGAGAAGGA GCTGAAACGG GAGCCAGCTG
          GTGGCACCAC GACGAGGCAC CCCTCTTCCT CGACTTTGCC CTCGGTCGAC
                          hICAM
          ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
    3551  TGGGGGAGCC CGCTGAGGTC ACGACCACGG TGCTGGTGAG GAGAGATCAC
          ACCCCCTCGG GCGACTCCAG TGCTGGTGCC ACGACCACTC CTCTCTAGTG
                          hICAM
          ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
    3601  CATGGAGCCA ATTTCTCGTG CCGCACTGAA CTGGACCTGC GGCCCCAAGG
          GTACCTCGGT TAAAGAGCAC GGCGTGACTT GACCTGGACG CCGGGGTTCC
                          hICAM
          ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
    3651  GCTGGAGCTG TTTGAGAACA CCTCGGCCCC CTACCAGCTC CAGACCTTTG
          CGACCTCGAC AAACTCTTGT GGAGCCGGGG GATGGTCGAG GTCTGGAAAC
                          hICAM
          ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
    3701  TCCTGCCAGC GACTCCCCCA CAACTTGTCA GCCCCCGGGT CCTAGAGGTG
          AGGACGGTCG CTGAGGGGGT GTTGAACAGT CGGGGGCCCA GGATCTCCAC
                          hICAM
          ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
    3751  GACACGCAGG GGACCGTGGT CTGTTCCCTG GACGGGCTGT TCCCAGTCTC
          CTGTGCGTCC CCTGGCACCA GACAAGGGAC CTGCCCGACA AGGGTCAGAG
                          hICAM
          ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
    3801  GGAGGCCCAG GTCCACCTGG CACTGGGGGA CCAGAGGTTG AACCCCACAG
          CCTCCGGGTC CAGGTGGACC GTGACCCCCT GGTCTCCAAC TTGGGGTGTC
                          hICAM
          ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
    3851  TCACCTATGG CAACGACTCC TTCTCGGCCA AGGCCTCAGT CAGTGTGACC
          AGTGGATACC GTTGCTGAGG AAGAGCCGGT TCCGGAGTCA GTCACACTGG
                          hICAM
          ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
    3901  GCAGAGGACG AGGGCACCCA GCGGCTGACG TGTGCAGTAA TACTGGGGAA
          CGTCTCCTGC TCCCGTGGGT CGCCGACTGC ACACGTCATT ATGACCCCTT
                          hICAM
          ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
    3951  CCAGAGCCAG GAGACACTGC AGACAGTGAC CATCTACAGC TTTCCGGCGC
          GGTCTCGGTC CTCTGTGACG TCTGTCACTG GTAGATGTCG AAAGGCCGCG
                          hICAM
          ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
    4001  CCAACGTGAT TCTGACGAAG CCAGAGGTCT CAGAAGGGAC CGAGGTGACA
          GGTTGCACTA AGACTGCTTC GGTCTCCAGA GTCTTCCCTG GCTCCACTGT
                          hICAM
          ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
    4051  GTGAAGTGTG AGGCCCACCC TAGAGCCAAG GTGACGCTGA ATGGGGTTCC
          CACTTCACAC TCCGGGTGGG ATCTCGGTTC CACTGCGACT TACCCCAAGG
                          hICAM
          ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
    4101  AGCCCAGCCA CTGGGCCCGA GGGCCCAGCT CCTGCTGAAG GCCACCCCAG
          TCGGGTCGGT GACCCGGGCT CCCGGGTCGA GGACGACTTC CGGTGGGGTC
                          hICAM
          ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
    4151  AGGACAACGG GCGCAGCTTC TCCTGCTCTG CAACCCTGGA GGTGGCCGGC
          TCCTGTTGCC CGCGTCGAAG AGGACGAGAC GTTGGGACCT CCACCGGCCG
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                                hICAM
                ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
          4201  CAGCTTATAC ACAAGAACCA GACCCGGGAG CTTCGTGTCC TGTATGGCCC
                GTCGAATATG TGTTCTTGGT CTGGGCCCTC GAAGCACAGG ACATACCGGG
5                               hICAM
                ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
          4251  CCGACTGGAC GAGAGGGATT GTCCGGGAAA CTGGACGTGG CCAGAAAATT
                GGCTGACCTG CTCTCCCTAA CAGGCCCTTT GACCTGCACC GGTCTTTTAA
                                hICAM
10              ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
          4301  CCCAGCAGAC TCCAATGTGC CAGGCTTGGG GGAACCCATT GCCCGAGCTC
                GGGTCGTCTG AGGTTACACG GTCCGAACCC CCTTGGGTAA CGGGCTCGAG
                                hICAM
15              ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
          4351  AAGTGTCTAA AGGATGGCAC TTTCCCACTG CCCATCGGGG AATCAGTGAC
                TTCACAGATT TCCTACCGTG AAAGGGTGAC GGGTAGCCCC TTAGTCACTG
                                hICAM
                ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
          4401  TGTCACTCGA GATCTTGAGG GCACCTACCT CTGTCGGGCC AGGAGCACTC
20              ACAGTGAGCT CTAGAACTCC CGTGGATGGA GACAGCCCGG TCCTCGTGAG
                                hICAM
                ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
          4451  AAGGGGAGGT CACCCGCGAG GTGACCGTGA ATGTGCTCTC CCCCCGGTAT
                TTCCCCTCCA GTGGGCGCTC CACTGGCACT TACACGAGAG GGGGGCCATA
25                              hICAM
                ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
          4501  GAGATTGTCA TCATCACTGT GGTAGCAGCC GCAGTCATAA TGGGCACTGC
                CTCTAACAGT AGTAGTGACA CCATCGTCGG CGTCAGTATT ACCCGTGACG
                                hICAM
30              ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
          4551  AGGCCTCAGC ACGTACCTCT ATAACCGCCA GCGGAAGATC AAGAAATACA
                TCCGGAGTCG TGCATGGAGA TATTGGCGGT CGCCTTCTAG TTCTTTATGT
                                hICAM
                ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
35        4601  GACTACAACA GGCCCAAAAA GGGACCCCCA TGAAACCGAA CACACAAGCC
                CTGATGTTGT CCGGGTTTTT CCCTGGGGGT ACTTTGGCTT GTGTGTTCGG
                  hICAM                                  sE/L Pr.
                ~~~~~~~~~~~~~                  ~~~~~~~~~~~~~~~~~~~~~~~~
          4651  ACGCCTCCCT GAGCATGCAT GTAGCTTAAA AATTGAAATT TTATTTTTTT
40              TGCGGAGGGA CTCGTACGTA CATCGAATTT TTAACTTTAA AATAAAAAAA
                  sE/L Pr.
                ~~~~~~~~~~~~~~~~~~
          4701  TTTTTGGAAT ATAAATAAGC TCGAAGTCGA AATTCCTGCA GCCCGGGGCC
                AAAAACCTTA TATTTATTCG AGCTTCAGCT TTAAGGACGT CGGGCCCCGG
45                              hB7.1
                ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
          4751  ATGGGCCACA CACGGAGGCA GGGAACATCA CCATCCAAGT GTCCATACCT
                TACCCGGTGT GTGCCTCCGT CCCTTGTAGT GGTAGGTTCA CAGGTATGGA
                                hB7.1
50              ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
          4801  CAATTTCTTT CAGCTCTTGG TGCTGGCTGG TCTTTCTCAC TTCTGTTCAG
                GTTAAAGAAA GTCGAGAACC ACGACCGACC AGAAAGAGTG AAGACAAGTC
                                hB7.1
                ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
55        4851  GTGTTATCCA CGTGACCAAG GAAGTGAAAG AAGTGGCAAC GCTGTCCTGT
                CACAATAGGT GCACTGGTTC CTTCACTTTC TTCACCGTTG CGACAGGACA
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                            hB7.1
      ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
4901  GGTCACAATG TTTCTGTTGA AGAGCTGGCA CAAACTCGCA TCTACTGGCA
      CCAGTGTTAC AAAGACAACT TCTCGACCGT GTTTGAGCGT AGATGACCGT
                            hB7.1
      ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
4951  AAAGGAGAAG AAAATGGTGC TGACTATGAT GTCTGGAGAC ATGAATATAT
      TTTCCTCTTC TTTTACCACG ACTGATACTA CAGACCTCTG TACTTATATA
                            hB7.1
      ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
5001  GGCCCGAGTA CAAGAACCGG ACCATCTTTG ATATCACTAA TAACCTCTCC
      CCGGGCTCAT GTTCTTGGCC TGGTAGAAAC TATAGTGATT ATTGGAGAGG
                            hB7.1
      ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
5051  ATTGTGATCC TGGCTCTGCG CCCATCTGAC GAGGGCACAT ACGAGTGTGT
      TAACACTAGG ACCGAGACGC GGGTAGACTG CTCCCGTGTA TGCTCACACA
                            hB7.1
      ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
5101  TGTTCTGAAG TATGAAAAAG ACGCTTTCAA GCGGGAACAC CTGGCTGAAG
      ACAAGACTTC ATACTTTTTC TGCGAAAGTT CGCCCTTGTG GACCGACTTC
                            hB7.1
      ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
5151  TGACGTTATC AGTCAAAGCT GACTTCCCTA CACCTAGTAT ATCTGACTTT
      ACTGCAATAG TCAGTTTCGA CTGAAGGGAT GTGGATCATA TAGACTGAAA
                            hB7.1
      ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
5201  GAAATTCCAA CTTCTAATAT TAGAAGGATA ATTTGCTCAA CCTCTGGAGG
      CTTTAAGGTT GAAGATTATA ATCTTCCTAT TAAACGAGTT GGAGACCTCC
                            hB7.1
      ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
5251  TTTTCCAGAG CCTCACCTCT CCTGGTTGGA AAATGGAGAA GAATTAAATG
      AAAAGGTCTC GGAGTGGAGA GGACCAACCT TTTACCTCTT CTTAATTTAC
                            hB7.1
      ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
5301  CCATCAACAC AACAGTTTCC CAAGATCCTG AAACTGAGCT CTATGCTGTT
      GGTAGTTGTG TTGTCAAAGG GTTCTAGGAC TTTGACTCGA GATACGACAA
                            hB7.1
      ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
5351  AGCAGCAAAC TGGATTTCAA TATGACAACC AACCACAGCT TCATGTGTCT
      TCGTCGTTTG ACCTAAAGTT ATACTGTTGG TTGGTGTCGA AGTACACAGA
                            hB7.1
      ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
5401  CATCAAGTAT GGACATTTAA GAGTGAATCA GACCTTCAAC TGGAATACAA
      GTAGTTCATA CCTGTAAATT CTCACTTAGT CTGGAAGTTG ACCTTATGTT
                            hB7.1
      ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
5451  CCAAGCAAGA GCATTTTCCT GATAACCTGC TCCCATCCTG GGCCATTACC
      GGTTCGTTCT CGTAAAAGGA CTATTGGACG AGGGTAGGAC CCGGTAATGG
                            hB7.1
      ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
5501  TTAATCTCAG TAAATGGAAT TTTCGTGATA TGCTGCCTGA CCTACTGCTT
      AATTAGAGTC ATTTACCTTA AAAGCACTAT ACGACGGACT GGATGACGAA
                            hB7.1
      ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
5551  TGCCCCACGC TGCAGAGAGA GAAGGAGGAA TGAGAGATTG AGAAGGGAAA
      ACGGGGTGCG ACGTCTCTCT CTTCCTCCTT ACTCTCTAAC TCTTCCCTTT
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hB7.1
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5601 GTGTACGCCC TGTATAAAAG CTTTCTAGGT TTTTGTTTAG GGCTGCAGGA
CACATGCGGG ACATATTTTC GAAAGATCCA AAAACAAATC CCGACGTCCT

5651 ATTCCTCGAG GGATCCCGAT TTTTATGACT AGTTAATCAA ATAAAAAGCA
TAAGGAGCTC CCTAGGGCTA AAAATACTGA TCAATTAGTT TATTTTTCGT

Right Arm

5701 TACAAGCTAT TGCTTCGCTA TCGTTACAAA ATGGCAGGAA TTTTGTGTAA
ATGTTCGATA ACGAAGCGAT AGCAATGTTT TACCGTCCTT AAAACACATT
~~~~~~
Right Arm

5751 ACTAAGCCAC ATACTTGCCA ATGAAAAAAA TAGTAGAAAG GATACTATTT
TGATTCGGTG TATGAACGGT TACTTTTTTT ATCATCTTTC CTATGATAAA
~~~~~~
Right Arm

5801 TAATGGGATT AGATGTTAAG GTTCCTTGGG ATTATAGTAA CTGGGCATCT
ATTACCCTAA TCTACAATTC CAAGGAACCC TAATATCATT GACCCGTAGA
~~~~~~
Right Arm

5851 GTTAACTTTT ACGACGTTAG GTTAGATACT GATGTTACAG ATTATAATAA
CAATTGAAAA TGCTGCAATC CAATCTATGA CTACAATGTC TAATATTATT
~~~~~~
Right Arm

5901 TGTTACAATA AAATACATGA CAGGATGTGA TATTTTTCCT CATATAACTC
ACAATGTTAT TTTATGTACT GTCCTACACT ATAAAAAGGA GTATATTGAG
~~~~~~
Right Arm

5951 TTGGAATAGC AAATATGGAT CAATGTGATA GATTTGAAAA TTTCAAAAAG
AACCTTATCG TTTATACCTA GTTACACTAT CTAAACTTTT AAAGTTTTTC
~~~~~~
Right Arm

6001 CAAATAACTG ATCAAGATTT ACAGACTATT TCTATAGTCT GTAAAGAAGA
GTTTATTGAC TAGTTCTAAA TGTCTGATAA AGATATCAGA CATTTCTTCT
~~~~~~
Right Arm

6051 GATGTGTTTT CCTCAGAGTA ACGCCTCTAA ACAGTTGGGA GCGAAAGGAT
CTACACAAAA GGAGTCTCAT TGCGGAGATT TGTCAACCCT CGCTTTCCTA
~~~~~~
Right Arm

6101 GCGCTGTAGT TATGAAACTG GAGGTATCTG ATGAACTTAG AGCCCTAAGA
CGCGACATCA ATACTTTGAC CTCCATAGAC TACTTGAATC TCGGGATTCT
~~~~~~
Right Arm

6151 AATGTTCTGC TGAATGCGGT ACCCTGTTCG AAGGACGTGT TTGGTGATAT
TTACAAGACG ACTTACGCCA TGGGACAAGC TTCCTGCACA AACCACTATA
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Right Arm

6201 CACAGTAGAT AATCCGTGGA ATCCTCACAT AACAGTAGGA TATGTTAAGG
GTGTCATCTA TTAGGCACCT TAGGAGTGTA TTGTCATCCT ATACAATTCC
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Right Arm

6251 AGGACGATGT CGAAAACAAG AAACGCCTAA TGGAGTGCAT GTCCAAGTTT
TCCTGCTACA GCTTTTGTTC TTTGCGGATT ACCTCACGTA CAGGTTCAAA
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Right Arm
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6301    AGGGGGCAAG AAATACAAGT TCTAGGATGG TATTAATAAG TATCTAAGTA
        TCCCCCGTTC TTTATGTTCA AGATCCTACC ATAATTATTC ATAGATTCAT
        ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
                            Right Arm
6351    TTTGGTATAA TTTATTAAAT AGTATAATTA TAACAAATAA TAAATAACAT
        AAACCATATT AAATAATTTA TCATATTAAT ATTGTTTATT ATTTATTGTA
        ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
                            Right Arm
6401    GATAACGGTT TTTATTAGAA TAAAATAGAG ATAATATCAT AATGATATAT
        CTATTGCCAA AAATAATCTT ATTTTATCTC TATTATAGTA TTACTATATA
        ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
                            Right Arm
6451    AATACTTCAT TACCAGAAAT GAGTAATGGA AGACTTATAA ATGAACTGCA
        TTATGAAGTA ATGGTCTTTA CTCATTACCT TCTGAATATT TACTTGACGT
        ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
                            Right Arm
6501    TAAAGCTATA AGGTATAGAG ATATAAATTT AGTAAGGTAT ATACTTAAAA
        ATTTCGATAT TCCATATCTC TATATTTAAA TCATTCCATA TATGAATTTT
        ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
                            Right Arm
6551    AATGCAAATA CAATAACGTA AATATACTAT CAACGTCTTT GTATTTAGCC
        TTACGTTTAT GTTATTGCAT TTATATGATA GTTGCAGAAA CATAAATCGG
        ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
                            Right Arm
6601    GTAAGTATTT CTGATATAGA AATGGTAAAA TTATTACTAG AACACGGTGC
        CATTCATAAA GACTATATCT TTACCATTTT AATAATGATC TTGTGCCACG
        ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
                            Right Arm
6651    CGATATTTTA AAATGTAAAA ATCCTCCTCT TCATAAAGCT GCTAGTTTAG
        GCTATAAAAT TTTACATTTT TAGGAGGAGA AGTATTTCGA CGATCAAATC
        ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
                            Right Arm
6701    ATAATACAGA AATTGCTAAA CTACTAATAG ATTCTGGCGC TGACATAGAA
        TATTATGTCT TTAACGATTT GATGATTATC TAAGACCGCG ACTGTATCTT
        ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
                            Right Arm
6751    CAGATACATT CTGGAAATAG TCCGTTATAT ATTTCTGTAT ATAGAAACAA
        GTCTATGTAA GACCTTTATC AGGCAATATA TAAAGACATA TATCTTTGTT
        ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
                            Right Arm
6801    TAAGTCATTA ACTAGATATT TATTAAAAAA AGGTGTTAAT TGTAATAGAT
        ATTCAGTAAT TGATCTATAA ATAATTTTTT TCCACAATTA ACATTATCTA
        ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
                            Right Arm
6851    TCTTTCTAAA TTATTACGAT GTACTGTATG ATAAGATATC TGATGATATG
        AGAAAGATTT AATAATGCTA CATGACATAC TATTCTATAG ACTACTATAC
        ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
                            Right Arm
6901    TATAAAATAT TTATAGATTT TAATATTGAT CTTAATATAC AAACTAGAAA
        ATATTTTATA AATATCTAAA ATTATAACTA GAATTATATG TTTGATCTTT
        ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
                            Right Arm
6951    TTTTGAAACT CCGTTACATT ACGCTATAAA GTATAAGAAT ATAGATTTAA
        AAAACTTTGA GGCAATGTAA TGCGATATTT CATATTCTTA TATCTAAATT
        ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
                            Right Arm
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7001  TTAGGATATT GTTAGATAAT AGTATTAAAA TAGATAAAAG TTTATTTTTG
      AATCCTATAA CAATCTATTA TCATAATTTT ATCTATTTTC AAATAAAAAC
      ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
                          Right Arm
7051  CATAAACAGT ATCTCATAAA GGCACTTAAA AATAATTGTA GTTACGATAT
      GTATTTGTCA TAGAGTATTT CCGTGAATTT TTATTAACAT CAATGCTATA
      ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
                          Right Arm
7101  AATAGCGTTA CTTATAAATC ACGGAGTGCC TATAAACGAA CAAGATGATT
      TTATCGCAAT GAATATTTAG TGCCTCACGG ATATTTGCTT GTTCTACTAA
      ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
                          Right Arm
7151  TAGGTAAAAC CCCATTACAT CATTCGGTAA TTAATAGAAG AAAAGATGTA
      ATCCATTTTG GGGTAATGTA GTAAGCCATT AATTATCTTC TTTTCTACAT
      ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
                          Right Arm
7201  ACAGCACTTC TGTTAAATCT AGGAGCTGAT ATAAACGTAA TAGATGACTG
      TGTCGTGAAG ACAATTTAGA TCCTCGACTA TATTTGCATT ATCTACTGAC
      ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
                          Right Arm
7251  TATGGGCAGT CCCTTACATT ACGCTGTTTC ACGTAACGAT ATCGAAACAA
      ATACCCGTCA GGGAATGTAA TGCGACAAAG TGCATTGCTA TAGCTTTGTT
      ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
                          Right Arm
7301  CAAAGACACT TTTAGAAAGA GGATCTAATG TTAATGTGGT TAATAATCAT
      GTTTCTGTGA AAATCTTTCT CCTAGATTAC AATTACACCA ATTATTAGTA
      ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
                          Right Arm
7351  ATAGATACCG TTCTAAATAT AGCTGTTGCA TCTAAAAACA AAACTATAGT
      TATCTATGGC AAGATTTATA TCGACAACGT AGATTTTTGT TTTGATATCA
      ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
                          Right Arm
7401  AAACTTATTA CTGAAGTACG GTACTGATAC AAAGTTGGTA GGATTAGATA
      TTTGAATAAT GACTTCATGC CATGACTATG TTTCAACCAT CCTAATCTAT
      ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
                          Right Arm
7451  AACATGTTAT TCACATAGCT ATAGAAATGA AAGATATTAA TATACTGAAT
      TTGTACAATA AGTGTATCGA TATCTTTACT TTCTATAATT ATATGACTTA
      ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
                          Right Arm
7501  GCGATCTTAT TATATGGTTG CTATGTAAAC GTCTATAATC ATAAAGGTTT
      CGCTAGAATA ATATACCAAC GATACATTTG CAGATATTAG TATTTCCAAA
      ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
                          Right Arm
7551  CACTCCTCTA TACATGGCAG TTAGTTCTAT GAAAACAGAA TTTGTTAAAC
      GTGAGGAGAT ATGTACCGTC AATCAAGATA CTTTTGTCTT AAACAATTTG
      ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
                          Right Arm
7601  TCTTACTTGA CCACGGTGCT TACGTAAATG CTAAAGCTAA GTTATCTGGA
      AGAATGAACT GGTGCCACGA ATGCATTTAC GATTTCGATT CAATAGACCT
      ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
                          Right Arm
7651  AATACTCCTT TACATAAAGC TATGTTATCT AATAGTTTTA ATAATATAAA
      TTATGAGGAA ATGTATTTCG ATACAATAGA TTATCAAAAT TATTATATTT
      ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
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                              Right Arm
      7701   ATTACTTTTA TCTTATAACG CCGACTATAA TTCTCTAAAT AATCACGGTA
             TAATGAAAAT AGAATATTGC GGCTGATATT AAGAGATTTA TTAGTGCCAT
             ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
                              Right Arm
      7751   ATACGCCTCT AACTTGTGTT AGCTTTTTAG ATGACAAGAT AGCTATTATG
             TATGCGGAGA TTGAACACAA TCGAAAAATC TACTGTTCTA TCGATAATAC
             ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
                              Right Arm
      7801   ATAATATCTA AAATGATGTT AGAAATATCT AAAAATCCTG AAATAGCTAA
             TATTATAGAT TTTACTACAA TCTTTATAGA TTTTTAGGAC TTTATCGATT
             ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
                              Right Arm
      7851   TTCAGAAGGT TTTATAGTAA ACATGGAACA TATAAACAGT AATAAAAGAC
             AAGTCTTCCA AAATATCATT TGTACCTTGT ATATTTGTCA TTATTTTCTG
             ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
                              Right Arm
      7901   TACTATCTAT AAAAGAATCA TGCGAAAAAG AACTAGATGT TATAACACAT
             ATGATAGATA TTTTCTTAGT ACGCTTTTTC TTGATCTACA ATATTGTGTA
             ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
                              Right Arm
      7951   ATAAAGTTAA ATTCTATATA TTCTTTTAAT ATCTTTCTTG ACAATAACAT
             TATTTCAATT TAAGATATAT AAGAAAATTA TAGAAAGAAC TGTTATTGTA
             ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
                              Right Arm
      8001   AGATCTTATG GTAAAGTTCG TAACTAATCC TAGAGTTAAT AAGATACCTG
             TCTAGAATAC CATTTCAAGC ATTGATTAGG ATCTCAATTA TTCTATGGAC
             ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
                              Right Arm
      8051   CATGTATACG TATATATAGG GAATTAATAC GGAAAAATAA ATCATTAGCT
             GTACATATGC ATATATATCC CTTAATTATG CCTTTTTATT TAGTAATCGA
             ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
                              Right Arm
      8101   TTTCATAGAC ATCAGCTAAT AGTTAAAGCT GTAAAAGAGA GTAAGAATCT
             AAAGTATCTG TAGTCGATTA TCAATTTCGA CATTTTCTCT CATTCTTAGA
             ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
                              Right Arm
      8151   AGGAATAATA GGTAGGTTAC CTATAGATAT CAAACATATA ATAATGGAAC
             TCCTTATTAT CCATCCAATG GATATCTATA GTTTGTATAT TATTACCTTG
             ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
                              Right Arm
      8201   TATTAAGTAA TAATGATTTA CATTCTGTTA TCACCAGCTG TTGTAACCCA
             ATAATTCATT ATTACTAAAT GTAAGACAAT AGTGGTCGAC AACATTGGGT
             ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
                              Right Arm
      8251   GTAGTATAAA GAGCTCCAGC TTTTGTTCCC TTTAGTGAGG GTTAATTCCG
             CATCATATTT CTCGAGGTCG AAAACAAGGG AAATCACTCC CAATTAAGGC
             ~~~~~~~~~~~~~~~~~~
                Right Arm
      8301   AGCTTGGCGT AATCATGGTC ATAGCTGTTT CCTGTGTGAA ATTGTTATCC
             TCGAACCGCA TTAGTACCAG TATCGACAAA GGACACACTT TAACAATAGG
      8351   GCTCACAATT CCACACAACA TACGAGCCGG AAGCATAAAG TGTAAAGCCT
             CGAGTGTTAA GGTGTGTTGT ATGCTCGGCC TTCGTATTTC ACATTTCGGA
      8401   GGGGTGCCTA ATGAGTGAGC TAACTCACAT TAATTGCGTT GCGCTCACTG
             CCCCACGGAT TACTCACTCG ATTGAGTGTA ATTAACGCAA CGCGAGTGAC
      8451   CCCGCTTTCC AGTCGGGAAA CCTGTCGTGC CAGCTGCATT AATGAATCGG
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      GGGCGAAAGG TCAGCCCTTT GGACAGCACG GTCGACGTAA TTACTTAGCC
8501  CCAACGCGCG GGGAGAGGCG GTTTGCGTAT TGGGCGCTCT TCCGCTTCCT
      GGTTGCGCGC CCCTCTCCGC CAAACGCATA ACCCGCGAGA AGGCGAAGGA
8551  CGCTCACTGA CTCGCTGCGC TCGGTCGTTC GGCTGCGGCG AGCGGTATCA
      GCGAGTGACT GAGCGACGCG AGCCAGCAAG CCGACGCCGC TCGCCATAGT
8601  GCTCACTCAA AGGCGGTAAT ACGGTTATCC ACAGAATCAG GGGATAACGC
      CGAGTGAGTT TCCGCCATTA TGCCAATAGG TGTCTTAGTC CCCTATTGCG
8651  AGGAAAGAAC ATGTGAGCAA AAGGCCAGCA AAAGGCCAGG AACCGTAAAA
      TCCTTTCTTG TACACTCGTT TTCCGGTCGT TTTCCGGTCC TTGGCATTTT
8701  AGGCCGCGTT GCTGGCGTTT TTCCATAGGC TCCGCCCCCC TGACGAGCAT
      TCCGGCGCAA CGACCGCAAA AAGGTATCCG AGGCGGGGGG ACTGCTCGTA
8751  CACAAAAATC GACGCTCAAG TCAGAGGTGG CGAAACCCGA CAGGACTATA
      GTGTTTTTAG CTGCGAGTTC AGTCTCCACC GCTTTGGGCT GTCCTGATAT
8801  AAGATACCAG GCGTTTCCCC CTGGAAGCTC CCTCGTGCGC TCTCCTGTTC
      TTCTATGGTC CGCAAAGGGG GACCTTCGAG GGAGCACGCG AGAGGACAAG
8851  CGACCCTGCC GCTTACCGGA TACCTGTCCG CCTTTCTCCC TTCGGGAAGC
      GCTGGGACGG CGAATGGCCT ATGGACAGGC GGAAAGAGGG AAGCCCTTCG
8901  GTGGCGCTTT CTCATAGCTC ACGCTGTAGG TATCTCAGTT CGGTGTAGGT
      CACCGCGAAA GAGTATCGAG TGCGACATCC ATAGAGTCAA GCCACATCCA
8951  CGTTCGCTCC AAGCTGGGCT GTGTGCACGA ACCCCCCGTT CAGCCCGACC
      GCAAGCGAGG TTCGACCCGA CACACGTGCT TGGGGGGCAA GTCGGGCTGG
9001  GCTGCGCCTT ATCCGGTAAC TATCGTCTTG AGTCCAACCC GGTAAGACAC
      CGACGCGGAA TAGGCCATTG ATAGCAGAAC TCAGGTTGGG CCATTCTGTG
9051  GACTTATCGC CACTGGCAGC AGCCACTGGT AACAGGATTA GCAGAGCGAG
      CTGAATAGCG GTGACCGTCG TCGGTGACCA TTGTCCTAAT CGTCTCGCTC
9101  GTATGTAGGC GGTGCTACAG AGTTCTTGAA GTGGTGGCCT AACTACGGCT
      CATACATCCG CCACGATGTC TCAAGAACTT CACCACCGGA TTGATGCCGA
9151  ACACTAGAAG GACAGTATTT GGTATCTGCG CTCTGCTGAA GCCAGTTACC
      TGTGATCTTC CTGTCATAAA CCATAGACGC GAGACGACTT CGGTCAATGG
9201  TTCGGAAAAA GAGTTGGTAG CTCTTGATCC GGCAAACAAA CCACCGCTGG
      AAGCCTTTTT CTCAACCATC GAGAACTAGG CCGTTTGTTT GGTGGCGACC
9251  TAGCGGTGGT TTTTTTGTTT GCAAGCAGCA GATTACGCGC AGAAAAAAAG
      ATCGCCACCA AAAAAACAAA CGTTCGTCGT CTAATGCGCG TCTTTTTTTC
9301  GATCTCAAGA AGATCCTTTG ATCTTTTCTA CGGGGTCTGA CGCTCAGTGG
      CTAGAGTTCT TCTAGGAAAC TAGAAAAGAT GCCCCAGACT GCGAGTCACC
9351  AACGAAAACT CACGTTAAGG GATTTTGGTC ATGAGATTAT CAAAAAGGAT
      TTGCTTTTGA GTGCAATTCC CTAAAACCAG TACTCTAATA GTTTTTCCTA
9401  CTTCACCTAG ATCCTTTTAA ATTAAAAATG AAGTTTTAAA TCAATCTAAA
      GAAGTGGATC TAGGAAAATT TAATTTTTAC TTCAAAATTT AGTTAGATTT
9451  GTATATATGA GTAAACTTGG TCTGACAGTT ACCAATGCTT AATCAGTGAG
      CATATATACT CATTTGAACC AGACTGTCAA TGGTTACGAA TTAGTCACTC
9501  GCACCTATCT CAGCGATCTG TCTATTTCGT TCATCCATAG TTGCCTGACT
      CGTGGATAGA GTCGCTAGAC AGATAAAGCA AGTAGGTATC AACGGACTGA
9551  CCCCGTCGTG TAGATAACTA CGATACGGGA GGGCTTACCA TCTGGCCCCA
      GGGGCAGCAC ATCTATTGAT GCTATGCCCT CCCGAATGGT AGACCGGGGT
9601  GTGCTGCAAT GATACCGCGA GACCCACGCT CACCGGCTCC AGATTTATCA
      CACGACGTTA CTATGGCGCT CTGGGTGCGA GTGGCCGAGG TCTAAATAGT
9651  GCAATAAACC AGCCAGCCGG AAGGGCCGAG CGCAGAAGTG GTCCTGCAAC
      CGTTATTTGG TCGGTCGGCC TTCCCGGCTC GCGTCTTCAC CAGGACGTTG
9701  TTTATCCGCC TCCATCCAGT CTATTAATTG TTGCCGGGAA GCTAGAGTAA
      AAATAGGCGG AGGTAGGTCA GATAATTAAC AACGGCCCTT CGATCTCATT
9751  GTAGTTCGCC AGTTAATAGT TTGCGCAACG TTGTTGCCAT TGCTACAGGC
      CATCAAGCGG TCAATTATCA AACGCGTTGC AACAACGGTA ACGATGTCCG
9801  ATCGTGGTGT CACGCTCGTC GTTTGGTATG GCTTCATTCA GCTCCGGTTC
      TAGCACCACA GTGCGAGCAG CAAACCATAC CGAAGTAAGT CGAGGCCAAG
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 9851  CCAACGATCA AGGCGAGTTA CATGATCCCC CATGTTGTGC AAAAAAGCGG
       GGTTGCTAGT TCCGCTCAAT GTACTAGGGG GTACAACACG TTTTTTCGCC
 9901  TTAGCTCCTT CGGTCCTCCG ATCGTTGTCA GAAGTAAGTT GGCCGCAGTG
       AATCGAGGAA GCCAGGAGGC TAGCAACAGT CTTCATTCAA CCGGCGTCAC
 9951  TTATCACTCA TGGTTATGGC AGCACTGCAT AATTCTCTTA CTGTCATGCC
       AATAGTGAGT ACCAATACCG TCGTGACGTA TTAAGAGAAT GACAGTACGG
10001  ATCCGTAAGA TGCTTTTCTG TGACTGGTGA GTACTCAACC AAGTCATTCT
       TAGGCATTCT ACGAAAAGAC ACTGACCACT CATGAGTTGG TTCAGTAAGA
10051  GAGAATAGTG TATGCGGCGA CCGAGTTGCT CTTGCCCGGC GTCAATACGG
       CTCTTATCAC ATACGCCGCT GGCTCAACGA GAACGGGCCG CAGTTATGCC
10101  GATAATACCG CGCCACATAG CAGAACTTTA AAAGTGCTCA TCATTGGAAA
       CTATTATGGC GCGGTGTATC GTCTTGAAAT TTTCACGAGT AGTAACCTTT
10151  ACGTTCTTCG GGGCGAAAAC TCTCAAGGAT CTTACCGCTG TTGAGATCCA
       TGCAAGAAGC CCCGCTTTTG AGAGTTCCTA GAATGGCGAC AACTCTAGGT
10201  GTTCGATGTA ACCCACTCGT GCACCCAACT GATCTTCAGC ATCTTTTACT
       CAAGCTACAT TGGGTGAGCA CGTGGGTTGA CTAGAAGTCG TAGAAAATGA
10251  TTCACCAGCG TTTCTGGGTG AGCAAAAACA GGAAGGCAAA ATGCCGCAAA
       AAGTGGTCGC AAAGACCCAC TCGTTTTTGT CCTTCCGTTT TACGGCGTTT
10301  AAAGGGAATA AGGGCGACAC GGAAATGTTG AATACTCATA CTCTTCCTTT
       TTTCCCTTAT TCCCGCTGTG CCTTTACAAC TTATGAGTAT GAGAAGGAAA
10351  TTCAATATTA TTGAAGCATT TATCAGGGTT ATTGTCTCAT GAGCGGATAC
       AAGTTATAAT AACTTCGTAA ATAGTCCCAA TAACAGAGTA CTCGCCTATG
10401  ATATTTGAAT GTATTTAGAA AAATAAACAA ATAGGGGTTC CGCGCACATT
       TATAAACTTA CATAAATCTT TTTATTTGTT TATCCCCAAG GCGCGTGTAA
10451  TCCCCGAAAA GTGCCACCTG AGGGGCTTTT CACGGTGGAC
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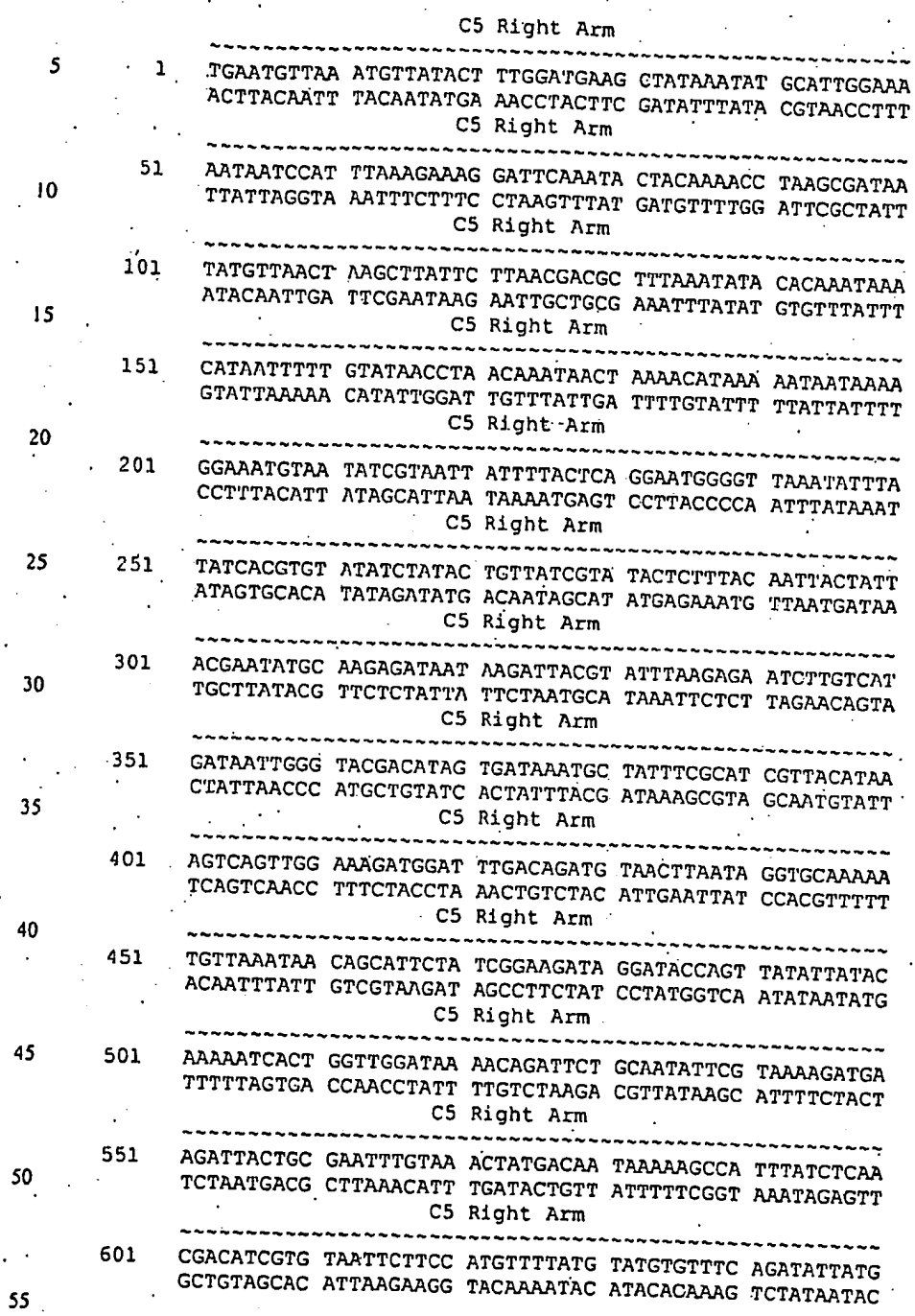
FIGURE 3: Donor plasmid p1132



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                          C5 Right Arm
                ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
          651   AGATTACTAT AAACTTTTTG TATACTTATA TTCCGTAAAC TATATTAATC
                TCTAATGATA TTTGAAAAAC ATATGAATAT AAGGCATTTG ATATAATTAG
                          C5 Right Arm
                ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
          701   ATGAAGAAAA TGAAAAAGTA TAGAAGCTGT TCACGAGCGG TTGTTGAAAA
                TACTTCTTTT ACTTTTTCAT ATCTTCGACA AGTGCTCGCC AACAACTTTT
                          C5 Right Arm
                ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
          751   CAACAAAATT ATACATTCAA GATGGCTTAC ATATACGTCT GTGAGGCTAT
                GTTGTTTTAA TATGTAAGTT CTACCGAATG TATATGCAGA CACTCCGATA
                          C5 Right Arm
                ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
          801   CATGGATAAT GACAATGCAT CTCTAAATAG GTTTTTGGAC AATGGATTCG
                GTACCTATTA CTGTTACGTA GAGATTTATC CAAAAACCTG TTACCTAAGC
                          C5 Right Arm
                ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
          851   ACCCTAACAC GGAATATGGT ACTCTACAAT CTCCTCTTGA AATGGCTGTA
                TGGGATTGTG CCTTATACCA TGAGATGTTA GAGGAGAACT TTACCGACAT
                          C5 Right Arm
                ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
          901   ATGTTCAAGA ATACCGAGGC TATAAAAATC TTGATGAGGT ATGGAGCTAA
                TACAAGTTCT TATGGCTCCG ATATTTTTAG AACTACTCCA TACCTCGATT
                          C5 Right Arm
                ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
          951   ACCTGTAGTT ACTGAATGCA CAACTTCTTG TCTGCATGAT GCGGTGTTGA
                TGGACATCAA TGACTTACGT GTTGAAGAAC AGACGTACTA CGCCACAACT
                          C5 Right Arm
                ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
         1001   GAGACGACTA CAAAATAGTG AAAGATCTGT TGAAGAATAA CTATGTAAAC
                CTCTGCTGAT GTTTTATCAC TTTCTAGACA ACTTCTTATT GATACATTTG
                          C5 Right Arm
                ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
         1051   AATGTTCTTT ACAGCGGAGG CTTTACTCCT TTGTGTTTGG CAGCTTACCT
                TTACAAGAAA TGTCGCCTCC GAAATGAGGA AACACAAACC GTCGAATGGA
                          C5 Right Arm
                ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
         1101   TAACAAAGTT AATTTGGTTA AACTTCTATT GGCTCATTCG GCGGATGTAG
                ATTGTTTCAA TTAAACCAAT TTGAAGATAA CCGAGTAAGC CGCCTACATC
                          C5 Right Arm
                ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
         1151   ATATTTCAAA CACGGATCGG TTAACTCCTC TACATATAGC CGTATCAAAT
                TATAAAGTTT GTGCCTAGCC AATTGAGGAG ATGTATATCG GCATAGTTTA
                          C5 Right Arm
                ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
         1201   AAAAATTTAA CAATGGTTAA ACTTCTATTG AACAAAGGTG CTGATACTGA
                TTTTTAAATT GTTACCAATT TGAAGATAAC TTGTTTCCAC GACTATGACT
                          C5 Right Arm
                ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
         1251   CTTGCTGGAT AACATGGGAT GTACTCCTTT AATGATCGCT GTACAATCTG
                GAACGACCTA TTGTACCCTA CATGAGGAAA TTACTAGCGA CATGTTAGAC
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                          C5 Right Arm
                ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
      1301      GAAATATTGA AATATGTAGC ACACTACTTA AAAAAAATAA AATGTCCAGA
                CTTTATAACT TTATACATCG TGTGATGAAT TTTTTTTATT TTACAGGTCT
                          C5 Right Arm
                ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
      1351      ACTGGGAAAA ATTGATCTTG CCAGCTGTAA TTCATGGTAG AAAAGAAGTG
                TGACCCTTTT TAACTAGAAC GGTCGACATT AAGTACCATC TTTTCTTCAC
                          C5 Right Arm
                ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
      1401      CTCAGGCTAC TTTTCAACAA AGGAGCAGAT GTAAACTACA TCTTTGAAAG
                GAGTCCGATG AAAAGTTGTT TCCTCGTCTA CATTTGATGT AGAAACTTTC
                          C5 Right Arm
                ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
      1451      AAATGGAAAA TCATATACTG TTTTGGAATT GATTAAAGAA AGTTACTCTG
                TTTACCTTTT AGTATATGAC AAAACCTTAA CTAATTTCTT TCAATGAGAC
                          C5 Right Arm
                ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
      1501      AGACACAAAA GAGGTAGCTG AAGTGGTACT CTCAAAGGTA CGTGACTAAT
                TCTGTGTTTT CTCCATCGAC TTCACCATGA GAGTTTCCAT GCACTGATTA
                                                          Repeat Region
                                                          ~~~~~~~~~~
      1551      TAGCTATAAA AAGGATCGGC CGCTCTAGAA CTAGTGGATC GGGTTCTTTA
                ATCGATATTT TTCCTAGCCG GCGAGATCTT GATCACCTAG CCCAAGAAAT
                          Repeat Region
                ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
      1601      TTCTATACTT AAAAAGTGAA AATAAATACA AAGGTTCTTG AGGGTTGTGT
                AAGATATGAA TTTTTCACTT TTATTTATGT TTCCAAGAAC TCCCAACACA
                          Repeat Region
                ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
      1651      TAAATTGAAA GCGAGAAATA ATCATAAATT ATTTCATTAT CGCGATATCC
                ATTTAACTTT CGCTCTTTAT TAGTATTTAA TAAAGTAATA GCGCTATAGG
                          Repeat Region
                ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
      1701      GTTAAGTTTG TATCGTACCC CGATCCCCCG AGCCATGCAG GCCGAAGGCC
                CAATTCAAAC ATAGCATGGG GCTAGGGGGC TCGGTACGTC CGGCTTCCGG
                          Repeat Region
                ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
      1751      GGGGCACAGG GGGTTCGACG GGCGATGCTG ATGGCCCAGG AGGCCCTGGC
                CCCCGTGTCC CCCAAGCTGC CCGCTACGAC TACCGGGTCC TCCGGGACCG
                          Repeat Region
                ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
      1801      ATTCCTGATG GCCCAGGGGG CAATGCTGGC GGCCCAGGAG AGGCGGGTGC
                TAAGGACTAC CGGGTCCCCC GTTACGACCG CCGGGTCCTC TCCGCCCACG
                          Repeat Region
                ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
      1851      CACGGGCGGC AGAGGTCCCC GGGGCGCAGG GGCAGCAAGG GCCTCGGGGC
                GTGCCCGCCG TCTCCAGGGG CCCCGCGTCC CCGTCGTTCC CGGAGCCCCG
                          Repeat Region
                ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
      1901      CGGGAGGAGG CGCCCCGCGG GGTCCGCATG GCGGCGCGGC TTCAGGGCTG
                GCCCTCCTCC GCGGGGCGCC CCAGGCGTAC CGCCGCGCCG AAGTCCCGAC
                          Repeat Region
                ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
      1951      AATGGATGCT GCAGATGCGG GGCCAGGGGG CCGGAGAGCC GCCTGCTTGA
                TTACCTACGA CGTCTACGCC CCGGTCCCCC GGCCTCTCGG CGGACGAACT
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                Repeat Region
              ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
     2001     GTTCTACCTC GCCATGCCTT TCGCGACACC CATAGCTTGA TATCGAATTC
              CAAGATGGAG CGGTACGGAA AGCGCTGTGG GTATCGAACT ATAGCTTAAG
                                              C1B promoter
                                             ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
     2051     TAGGGGGATC CACTAGTTCT AGAGGATCAT TATTTAACGT AAACTAAATG
              ATCCCCCTAG GTGATCAAGA TCTCCTAGTA ATAAATTGCA TTTGATTTAC
                              C1B promoter
              ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
     2101     GAAAAGCTAT TTACAGGTAC ATACGGTGTT TTTCTGGAAT CAAATGATTC
              CTTTTCGATA AATGTCCATG TATGCCACAA AAAGACCTTA GTTTACTAAG
                              C1B promoter
              ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
     2151     TGATTTTGAG GATTTTATCA ATACAATAAT GACAGTGCTA ACTGGTAAAA
              ACTAAAACTC CTAAAATAGT TATGTTATTA CTGTCACGAT TGACCATTTT
                              C1B promoter
              ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
     2201     AAGAAAGCAA ACAATTATCA TGGCTAACAA TTTTTATTAT ATTTGTAGTA
              TTCTTTCGTT TGTTAATAGT ACCGATTGTT AAAAATAATA TAAACATCAT
                              C1B promoter
              ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
     2251     TGCATAGTGG TCTTTACGTT TCTTTATTTA AAGTTAATGT GTTAAGATTA
              ACGTATCACC AGAAATGCAA AGAAATAAAT TTCAATTACA CAATTCTAAT
                C1B promoter                          LacZ
              ~~~~~~~~~~~~~~~~~~~~          ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
     2301     AATGGAGTAA TTGGATCCCC CATCGATGGG GAATTCACTG GCCGTCGTTT
              TTACCTCATT AACCTAGGGG GTAGCTACCC CTTAAGTGAC CGGCAGCAAA
                                    LacZ
              ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
     2351     TACAACGTCG TGACTGGGAA AACCCTGGCG TTACCCAACT TAATCGCCTT
              ATGTTGCAGC ACTGACCCTT TTGGGACCGC AATGGGTTGA ATTAGCGGAA
                                    LacZ
              ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
     2401     GCAGCACATC CCCCTTTCGC CAGCTGGCGT AATAGCGAAG AGGCCCGCAC
              CGTCGTGTAG GGGGAAAGCG GTCGACCGCA TTATCGCTTC TCCGGGCGTG
                                    LacZ
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     2451     CGATCGCCCT TCCCAACAGT TGCGCAGCCT GAATGGCGAA TGGCGCTTTG
              GCTAGCGGGA AGGGTTGTCA ACGCGTCGGA CTTACCGCTT ACCGCGAAAC
                                    LacZ
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     2501     CCTGGTTTCC GGCACCAGAA GCGGTGCCGG AAAGCTGGCT GGAGTGCGAT
              GGACCAAAGG CCGTGGTCTT CGCCACGGCC TTTCGACCGA CCTCACGCTA
                                    LacZ
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     2551     CTTCCTGAGG CCGATACTGT CGTCGTCCCC TCAAACTGGC AGATGCACGG
              GAAGGACTCC GGCTATGACA GCAGCAGGGG AGTTTGACCG TCTACGTGCC
                                    LacZ
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     2601     TTACGATGCG CCCATCTACA CCAACGTGAC CTATCCCATT ACGGTCAATC
              AATGCTACGC GGGTAGATGT GGTTGCACTG GATAGGGTAA TGCCAGTTAG
                                    LacZ
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     2651     CGCCGTTTGT TCCCACGGAG AATCCGACGG GTTGTTACTC GCTCACATTT
              GCGGCAAACA AGGGTGCCTC TTAGGCTGCC CAACAATGAG CGAGTGTAAA
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LacZ

2701 AATGTTGATG AAAGCTGGCT ACAGGAAGGC CAGACGCGAA TTATTTTTGA
TTACAACTAC TTTCGACCGA TGTCCTTCCG GTCTGCGCTT AATAAAAACT

LacZ

2751 TGGCGTTAAC TCGGCGTTTC ATCTGTGGTG CAACGGGCGC TGGGTCGGTT
ACCGCAATTG AGCCGCAAAG TAGACACCAC GTTGCCCGCG ACCCAGCCAA

LacZ

2801 ACGGCCAGGA CAGTCGTTTG CCGTCTGAAT TTGACCTGAG CGCATTTTTA
TGCCGGTCCT GTCAGCAAAC GGCAGACTTA AACTGGACTC GCGTAAAAAT

LacZ

2851 CGCGCCGGAG AAAACCGCCT CGCGGTGATG GTGCTGCGCT GGAGTGACGG
GCGCGGCCTC TTTTGGCGGA GCGCCACTAC CACGACGCGA CCTCACTGCC

LacZ

2901 CAGTTATCTG GAAGATCAGG ATATGTGGCG GATGAGCGGC ATTTTCCGTG
GTCAATAGAC CTTCTAGTCC TATACACCGC CTACTCGCCG TAAAAGGCAC

LacZ

2951 ACGTCTCGTT GCTGCATAAA CCGACTACAC AAATCAGCGA TTTCCATGTT
TGCAGAGCAA CGACGTATTT GGCTGATGTG TTTAGTCGCT AAAGGTACAA

LacZ

3001 GCCACTCGCT TTAATGATGA TTTCAGCCGC GCTGTACTGG AGGCTGAAGT
CGGTGAGCGA AATTACTACT AAAGTCGGCG CGACATGACC TCCGACTTCA

LacZ

3051 TCAGATGTGC GGCGAGTTGC GTGACTACCT ACGGGTAACA GTTTCTTTAT
AGTCTACACG CCGCTCAACG CACTGATGGA TGCCCATTGT CAAAGAAATA

LacZ

3101 GGCAGGGTGA AACGCAGGTC GCCAGCGGCA CCGCGCCTTT CGGCGGTGAA
CCGTCCCACT TTGCGTCCAG CGGTCGCCGT GGCGCGGAAA GCCGCCACTT

LacZ

3151 ATTATCGATG AGCGTGGTGG TTATGCCGAT CGCGTCACAC TACGTCTGAA
TAATAGCTAC TCGCACCACC AATACGGCTA GCGCAGTGTG ATGCAGACTT

LacZ

3201 CGTCGAAAAC CCGAAACTGT GGAGCGCCGA AATCCCGAAT CTCTATCGTG
GCAGCTTTTG GGCTTTGACA CCTCGCGGCT TTAGGGCTTA GAGATAGCAC

LacZ

3251 CGGTGGTTGA ACTGCACACC GCCGACGGCA CGCTGATTGA AGCAGAAGCC
GCCACCAACT TGACGTGTGG CGGCTGCCGT GCGACTAACT TCGTCTTCGG

LacZ

3301 TGCGATGTCG GTTTCCGCGA GGTGCGGATT GAAAATGGTC TGCTGCTGCT
ACGCTACAGC CAAAGGCGCT CCACGCCTAA CTTTTACCAG ACGACGACGA

LacZ

3351 GAACGGCAAG CCGTTGCTGA TTCGAGGCGT TAACCGTCAC GAGCATCATC
CTTGCCGTTC GGCAACGACT AAGCTCCGCA ATTGGCAGTG CTCGTAGTAG

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                                LacZ
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      3401      CTCTGCATGG TCAGGTCATG GATGAGCAGA CGATGGTGCA GGATATCCTG
                GAGACGTACC AGTCCAGTAC CTACTCGTCT GCTACCACGT CCTATAGGAC
                                LacZ
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      3451      CTGATGAAGC AGAACAACTT TAACGCCGTG CGCTGTTCGC ATTATCCGAA
                GACTACTTCG TCTTGTTGAA ATTGCGGCAC GCGACAAGCG TAATAGGCTT
                                LacZ
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      3501      CCATCCGCTG TGGTACACGC TGTGCGACCG CTACGGCCTG TATGTGGTGG
                GGTAGGCGAC ACCATGTGCG ACACGCTGGC GATGCCGGAC ATACACCACC
                                LacZ
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      3551      ATGAAGCCAA TATTGAAACC CACGGCATGG TGCCAATGAA TCGTCTGACC
                TACTTCGGTT ATAACTTTGG GTGCCGTACC ACGGTTACTT AGCAGACTGG
                                LacZ
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      3601      GATGATCCGC GCTGGCTACC GGCGATGAGC GAACGCGTAA CGCGAATGGT
                CTACTAGGCG CGACCGATGG CCGCTACTCG CTTGCGCATT GCGCTTACCA
                                LacZ
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      3651      GCAGCGCGAT CGTAATCACC CGAGTGTGAT CATCTGGTCG CTGGGGAATG
                CGTCGCGCTA GCATTAGTGG GCTCACACTA GTAGACCAGC GACCCCTTAC
                                LacZ
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      3701      AATCAGGCCA CGGCGCTAAT CACGACGCGC TGTATCGCTG GATCAAATCT
                TTAGTCCGGT GCCGCGATTA GTGCTGCGCG ACATAGCGAC CTAGTTTAGA
                                LacZ
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      3751      GTCGATCCTT CCCGCCCGGT GCAGTATGAA GGCGGCGGAG CCGACACCAC
                CAGCTAGGAA GGGCGGGCCA CGTCATACTT CCGCCGCCTC GGCTGTGGTG
                                LacZ
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      3801      GGCCACCGAT ATTATTTGCC CGATGTACGC GCGCGTGGAT GAAGACCAGC
                CCGGTGGCTA TAATAAACGG GCTACATGCG CGCGCACCTA CTTCTGGTCG
                                LacZ
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      3851      CCTTCCCGGC TGTGCCGAAA TGGTCCATCA AAAAATGGCT TTCGCTACCT
                GGAAGGGCCG ACACGGCTTT ACCAGGTAGT TTTTTACCGA AAGCGATGGA
                                LacZ
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      3901      GGAGAGACGC GCCCGCTGAT CCTTTGCGAA TACGCCCACG CGATGGGTAA
                CCTCTCTGCG CGGGCGACTA GGAAACGCTT ATGCGGGTGC GCTACCCATT
                                LacZ
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      3951      CAGTCTTGGC GGTTTCGCTA AATACTGGCA GGCGTTTCGT CAGTATCCCC
                GTCAGAACCG CCAAAGCGAT TTATGACCGT CCGCAAAGCA GTCATAGGGG
                                LacZ
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      4001      GTTTACAGGG CGGCTTCGTC TGGGACTGGG TGGATCAGTC GCTGATTAAA
                CAAATGTCCC GCCGAAGCAG ACCCTGACCC ACCTAGTCAG CGACTAATTT
                                LacZ
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      4051      TATGATGAAA ACGGCAACCC GTGGTCGGCT TACGGCGGTG ATTTTGGCGA
                ATACTACTTT TGCCGTTGGG CACCAGCCGA ATGCCGCCAC TAAAACCGCT
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                                   LacZ
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          4101  TACGCCGAAC GATCGCCAGT TCTGTATGAA CGGTCTGGTC TTTGCCGACC
                ATGCGGCTTG CTAGCGGTCA AGACATACTT GCCAGACCAG AAACGGCTGG
                                   LacZ
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          4151  GCACGCCGCA TCCAGCGCTG ACGGAAGCAA AACACCAGCA GCAGTTTTTC
                CGTGCGGCGT AGGTCGCGAC TGCCTTCGTT TTGTGGTCGT CGTCAAAAAG
                                   LacZ
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          4201  CAGTTCCGTT TATCCGGGCA AACCATCGAA GTGACCAGCG AATACCTGTT
                GTCAAGGCAA ATAGGCCCGT TTGGTAGCTT CACTGGTCGC TTATGGACAA
                                   LacZ
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          4251  CCGTCATAGC GATAACGAGC TCCTGCACTG GATGGTGGCG CTGGATGGTA
                GGCAGTATCG CTATTGCTCG AGGACGTGAC CTACCACCGC GACCTACCAT
                                   LacZ
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          4301  AGCCGCTGGC AAGCGGTGAA GTGCCTCTGG ATGTCGCTCC ACAAGGTAAA
                TCGGCGACCG TTCGCCACTT CACGGAGACC TACAGCGAGG TGTTCCATTT
                                   LacZ
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          4351  CAGTTGATTG AACTGCCTGA ACTACCGCAG CCGGAGAGCG CCGGGCAACT
                GTCAACTAAC TTGACGGACT TGATGGCGTC GGCCTCTCGC GGCCCGTTGA
                                   LacZ
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          4401  CTGGCTCACA GTACGCGTAG TGCAACCGAA CGCGACCGCA TGGTCAGAAG
                GACCGAGTGT CATGCGCATC ACGTTGGCTT GCGCTGGCGT ACCAGTCTTC
                                   LacZ
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          4451  CCGGGCACAT CAGCGCCTGG CAGCAGTGGC GTCTGGCGGA AAACCTCAGT
                GGCCCGTGTA GTCGCGGACC GTCGTCACCG CAGACCGCCT TTTGGAGTCA
                                   LacZ
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          4501  GTGACGCTCC CCGCCGCGTC CCACGCCATC CCGCATCTGA CCACCAGCGA
                CACTGCGAGG GGCGGCGCAG GGTGCGGTAG GGCGTAGACT GGTGGTCGCT
                                   LacZ
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          4551  AATGGATTTT TGCATCGAGC TGGGTAATAA GCGTTGGCAA TTTAACCGCC
                TTACCTAAAA ACGTAGCTCG ACCCATTATT CGCAACCGTT AAATTGGCGG
                                   LacZ
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          4601  AGTCAGGCTT TCTTTCACAG ATGTGGATTG GCGATAAAAA ACAACTGCTG
                TCAGTCCGAA AGAAAGTGTC TACACCTAAC CGCTATTTTT TGTTGACGAC
                                   LacZ
                ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
          4651  ACGCCGCTGC GCGATCAGTT CACCCGTGCA CCGCTGGATA ACGACATTGG
                TGCGGCGACG CGCTAGTCAA GTGGGCACGT GGCGACCTAT TGCTGTAACC
                                   LacZ
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          4701  CGTAAGTGAA GCGACCCGCA TTGACCCTAA CGCCTGGGTC GAACGCTGGA
                GCATTCACTT CGCTGGGCGT AACTGGGATT GCGGACCCAG CTTGCGACCT
                                   LacZ
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          4751  AGGCGGCGGG CCATTACCAG GCCGAAGCAG CGTTGTTGCA GTGCACGGCA
                TCCGCCGCCC GGTAATGGTC CGGCTTCGTC GCAACAACGT CACGTGCCGT
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                                LacZ
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      4801      GATACACTTG CTGATGCGGT GCTGATTACG ACCGCTCACG CGTGGCAGCA
                CTATGTGAAC GACTACGCCA CGACTAATGC TGGCGAGTGC GCACCGTCGT
                                LacZ
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      4851      TCAGGGGAAA ACCTTATTTA TCAGCCGGAA AACCTACCGG ATTGATGGTA
                AGTCCCCTTT TGGAATAAAT AGTCGGCCTT TTGGATGGCC TAACTACCAT
                                LacZ
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      4901      GTGGTCAAAT GGCGATTACC GTTGATGTTG AAGTGGCGAG CGATACACCG
                CACCAGTTTA CCGCTAATGG CAACTACAAC TTCACCGCTC GCTATGTGGC
                                LacZ
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      4951      CATCCGGCGC GGATTGGCCT GAACTGCCAG CTGGCGCAGG TAGCAGAGCG
                GTAGGCCGCG CCTAACCGGA CTTGACGGTC GACCGCGTCC ATCGTCTCGC
                                LacZ
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      5001      GGTAAACTGG CTCGGATTAG GGCCGCAAGA AAACTATCCC GACCGCCTTA
                CCATTTGACC GAGCCTAATC CCGGCGTTCT TTTGATAGGG CTGGCGGAAT
                                LacZ
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      5051      CTGCCGCCTG TTTTGACCGC TGGGATCTGC CATTGTCAGA CATGTATACC
                GACGGCGGAC AAAACTGGCG ACCCTAGACG GTAACAGTCT GTACATATGG
                                LacZ
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      5101      CCGTACGTCT TCCCGAGCGA AAACGGTCTG CGCTGCGGGA CGCGCGAATT
                GGCATGCAGA AGGGCTCGCT TTTGCCAGAC GCGACGCCCT GCGCGCTTAA
                                LacZ
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      5151      GAATTATGGC CCACACCAGT GGCGCGGCGA CTTCCAGTTC AACATCAGCC
                CTTAATACCG GGTGTGGTCA CCGCGCCGCT GAAGGTCAAG TTGTAGTCGG
                                LacZ
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      5201      GGTACAGTCA ACAGCAATTG ATGGAAACCA GCCATTCGCC ATCTGCTGCA
                CCATGTCAGT TGTCGTTAAC TACCTTTGGT CGGTAAGCGG TAGACGACGT
                                LacZ
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      5251      CGCGGAAGAG GCACATGGCT GAATATCGAC GGTTTCCATA TGGGGATTGG
                GCGCCTTCTC CGTGTACCGA CTTATAGCTG CCAAAGGTAT ACCCCTAACC
                                LacZ
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      5301      TGGCGACGAC TCCTGGAGCC CGTCAGTATC GGCGGAATTC CAGCTGAGCG
                ACCGCTGCTG AGGACCTCGG GCAGTCATAG CCGCCTTAAG GTCGACTCGC
                                LacZ
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      5351      CCGGTCGCTA CCATTACCAG TTGGTCTGGT GTCAAAAATA ATAATAACCG
                GGCCAGCGAT GGTAATGGTC AACCAGACCA CAGTTTTTAT TATTATTGGC
      5401      GGCAGGGGGG ATCCGGAGCT TATCGCAGAT CAATTCGATA TCAAGCTTAT
                CCGTCCCCCC TAGGCCTCGA ATAGCGTCTA GTTAAGCTAT AGTTCGAATA
                                                    H6  Promoter
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      5451      CGATACCGTC GACGGTATCG ATAAGCTCTA GTGGAGGGTT CTTTATTCTA
                GCTATGGCAG CTGCCATAGC TATTCGAGAT CACCTCCCAA GAAATAAGAT
                                H6  Promoter
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5501   TACTTAAAAA GTGAAAATAA ATACAAAGGT TCTTGAGGGT TGTGTTAAAT
       ATGAATTTTT CACTTTTATT TATGTTTCCA AGAACTCCCA ACACAATTTA
                          H6  Promoter
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5551   TGAAAGCGAG AAATAATCAT AAATTATTTC ATTATCGCGA TATCCGTTAA
       ACTTTCGCTC TTTATTAGTA TTTAATAAAG TAATAGCGCT ATAGGCAATT
        H6  Promoter                              NYESO-1
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5601   GTTTGTATCG TACCCCCCCC GAGCCATGCA GGCCGAAGGC CGGGGCACAG
       CAAACATAGC ATGGGGGGGG CTCGGTACGT CCGGCTTCCG GCCCCGTGTC
                                NYESO-1
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5651   GGGGTTCGAC GGGCGATGCT GATGGCCCAG GAGGCCCTGG CATTCCTGAT
       CCCCAAGCTG CCCGCTACGA CTACCGGGTC CTCCGGGACC GTAAGGACTA
                                NYESO-1
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5701   GGCCCAGGGG GCAATGCTGG CGGCCCAGGA GAGGCGGGTG CCACGGGCGG
       CCGGGTCCCC CGTTACGACC GCCGGGTCCT CTCCGCCCAC GGTGCCCGCC
                                NYESO-1
       ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
5751   CAGAGGTCCC CGGGGCGCAG GGGCAGCAAG GGCCTCGGGG CCGGGAGGAG
       GTCTCCAGGG GCCCCGCGTC CCCGTCGTTC CCGGAGCCCC GGCCCTCCTC
                                NYESO-1
       ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
5801   GCGCCCCGCG GGGTCCGCAT GGCGGCGCGG CTTCAGGGCT GAATGGATGC
       CGCGGGGCGC CCCAGGCGTA CCGCCGCGCC GAAGTCCCGA CTTACCTACG
                                NYESO-1
       ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
5851   TGCAGATGCG GGGCCAGGGG GCCGGAGAGC CGCCTGCTTG AGTTCTACCT
       ACGTCTACGC CCCGGTCCCC CGGCCTCTCG GCGGACGAAC TCAAGATGGA
                                NYESO-1
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5901   CGCCATGCCT TTCGCGACAC CCATGGAAGC AGAGCTGGCC CGCAGGAGCC
       GCGGTACGGA AAGCGCTGTG GGTACCTTCG TCTCGACCGG GCGTCCTCGG
                                NYESO-1
       ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
5951   TGGCCCAGGA TGCCCCACCG CTTCCCGTGC CAGGGGTGCT TCTGAAGGAG
       ACCGGGTCCT ACGGGGTGGC GAAGGGCACG GTCCCCACGA AGACTTCCTC
                                NYESO-1
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6001   TTCACTGTGT CCGGCAACAT ACTGACTATC CGACTGACTG CTGCAGACCA
       AAGTGACACA GGCCGTTGTA TGACTGATAG GCTGACTGAC GACGTCTGGT
                                NYESO-1
       ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
6051   CCGCCAACTG CAGCTCTCCA TCAGCTCCTG TCTCCAGCAG CTTTCCCTGT
       GGCGGTTGAC GTCGAGAGGT AGTCGAGGAC AGAGGTCGTC GAAAGGGACA
                                NYESO-1
       ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
6101   TGATGTGGAT CACGCAGGTG TTTCTGCCCG TGTTTTTGGC TCAGCCTCCC
       ACTACACCTA GTGCGTCCAC AAAGACGGGC ACAAAAACCG AGTCGGAGGG
              NYESO-1
       ~~~~~~~~~~~~~~~~~~~~~~~~~~~~
6151   TCAGGGCAGA GGCGCTAAGT AATTAATTTT TTTTTGGGCT GCAGGATCGC
       AGTCCCGTCT CCGCGATTCA TTAATTAAAA AAAAACCCGA CGTCCTAGCG
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                              sE/L Promoter
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6201  TAGCAAAAAT TGAAATTTTA TTTTTTTTTT TTGGAATATA AATAAGCTCG
      ATCGTTTTTA ACTTTAAAAT AAAAAAAAAA AACCTTATAT TTATTCGAGC
                                      hTRP-2
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      sE/L Promoter
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6251  AAGCTCGAGC CATGAGCCCC CTTTGGTGGG GGTTTCTGCT CAGTTGCTTG
      TTCGAGCTCG GTACTCGGGG GAAACCACCC CCAAAGACGA GTCAACGAAC
                            hTRP-2
      ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
6301  GGCTGCAAAA TCCTGCCAGG AGCCCAGGGT CAGTTCCCCC GAGTCTGCAT
      CCGACGTTTT AGGACGGTCC TCGGGTCCCA GTCAAGGGGG CTCAGACGTA
                            hTRP-2
      ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
6351  GACGGTGGAC AGCCTAGTGA ACAAGGAGTG CTGCCCACGC CTGGGTGCAG
      CTGCCACCTG TCGGATCACT TGTTCCTCAC GACGGGTGCG GACCCACGTC
                            hTRP-2
      ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
6401  AGTCGGCCAA TGTCTGTGGC TCTCAGCAAG GCCGGGGGCA GTGCACAGAG
      TCAGCCGGTT ACAGACACCG AGAGTCGTTC CGGCCCCCGT CACGTGTCTC
                            hTRP-2
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6451  GTGCGAGCCG ACACAAGGCC CTGGAGTGGT CCCTACATCC TACGAAACCA
      CACGCTCGGC TGTGTTCCGG GACCTCACCA GGGATGTAGG ATGCTTTGGT
                            hTRP-2
      ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
6501  GGATGACCGT GAGCTGTGGC CAAGAAAATT CTTCCACCGG ACCTGCAAGT
      CCTACTGGCA CTCGACACCG GTTCTTTTAA GAAGGTGGCC TGGACGTTCA
                            hTRP-2
      ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
6551  GCACAGGAAA CTTTGCCGGC TATAATTGTG GAGACTGCAA GTTTGGCTGG
      CGTGTCCTTT GAAACGGCCG ATATTAACAC CTCTGACGTT CAAACCGACC
                            hTRP-2
      ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
6601  ACCGGTCCCA ACTGCGAGCG GAAGAAACCA CCAGTGATTC GGCAGAACAT
      TGGCCAGGGT TGACGCTCGC CTTCTTTGGT GGTCACTAAG CCGTCTTGTA
                            hTRP-2
      ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
6651  CCATTCCTTG AGTCCTCAGG AAAGAGAGCA GTTCTTGGGC GCCTTAGATC
      GGTAAGGAAC TCAGGAGTCC TTTCTCTCGT CAAGAACCCG CGGAATCTAG
                            hTRP-2
      ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
6701  TCGCGAAGAA GAGAGTACAC CCCGACTACG TGATCACCAC ACAACACTGG
      AGCGCTTCTT CTCTCATGTG GGGCTGATGC ACTAGTGGTG TGTTGTGACC
                            hTRP-2
      ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
6751  CTGGGCCTGC TTGGGCCCAA TGGAACCCAG CCGCAGTTTG CCAACTGCAG
      GACCCGGACG AACCCGGGTT ACCTTGGGTC GGCGTCAAAC GGTTGACGTC
                            hTRP-2
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6801  TGTTTATGAT TTCTTCGTGT GGCTCCATTA TTATTCTGTT AGAGATACAT
      ACAAATACTA AAGAAGCACA CCGAGGTAAT AATAAGACAA TCTCTATGTA
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                                  hTRP-2
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          6851    TATTAGGACC AGGACGCCCC TACAGGGCCA TAGATTTCTC ACATCAAGGA
                  ATAATCCTGG TCCTGCGGGG ATGTCCCGGT ATCTAAAGAG TGTAGTTCCT
                                  hTRP-2
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          6901    CCTGCATTTG TTACCTGGCA CCGGTACCAT TTGTTGTGTC TGGAAAGAGA
                  GGACGTAAAC AATGGACCGT GGCCATGGTA AACAACACAG ACCTTTCTCT
                                  hTRP-2
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          6951    TCTCCAGCGA CTCATTGGCA ATGAGTCTTT TGCTTTGCCC TACTGGAACT
                  AGAGGTCGCT GAGTAACCGT TACTCAGAAA ACGAAACGGG ATGACCTTGA
                                  hTRP-2
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          7001    TTGCCACTGG GAGGAACGAG TGTGATGTGT GTACAGACCA GCTGTTTGGG
                  AACGGTGACC CTCCTTGCTC ACACTACACA CATGTCTGGT CGACAAACCC
                                  hTRP-2
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          7051    GCAGCGAGAC CAGACGATCC GACTCTGATT AGTCGGAACT CAAGATTCTC
                  CGTCGCTCTG GTCTGCTAGG CTGAGACTAA TCAGCCTTGA GTTCTAAGAG
                                  hTRP-2
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          7101    CAGCTGGGAA ACTGTCTGTG ATAGCTTGGA TGACTACAAC CACCTGGTCA
                  GTCGACCCTT TGACAGACAC TATCGAACCT ACTGATGTTG GTGGACCAGT
                                  hTRP-2
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          7151    CCTTGTGCAA TGGAACCTAT GAAGGTTTGC TGAGAAGAAA TCAAATGGGA
                  GGAACACGTT ACCTTGGATA CTTCCAAACG ACTCTTCTTT AGTTTACCCT
                                  hTRP-2
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          7201    AGAAACAGCA TGAAATTGCC AACCTTAAAA GACATACGAG ATTGCCTGTC
                  TCTTTGTCGT ACTTTAACGG TTGGAATTTT CTGTATGCTC TAACGGACAG
                                  hTRP-2
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          7251    TCTCCAGAAG TTTGACAATC CTCCCTTCTT CCAGAACTCT ACCTTCAGTT
                  AGAGGTCTTC AAACTGTTAG GAGGGAAGAA GGTCTTGAGA TGGAAGTCAA
                                  hTRP-2
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          7301    TCAGGAATGC TTTGGAAGGG TTTGATAAAG CAGATGGGAC TCTGGATTCT
                  AGTCCTTACG AAACCTTCCC AAACTATTTC GTCTACCCTG AGACCTAAGA
                                  hTRP-2
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          7351    CAAGTGATGA GCCTTCATAA TTTGGTTCAT TCCTTCCTGA ACGGGACAAA
                  GTTCACTACT CGGAAGTATT AAACCAAGTA AGGAAGGACT TGCCCTGTTT
                                  hTRP-2
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          7401    CGCTTTGCCA CATTCAGCCG CCAATGATCC CATCTTCGTG GTGATTTCTA
                  GCGAAACGGT GTAAGTCGGC GGTTACTAGG GTAGAAGCAC CACTAAAGAT
                                  hTRP-2
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          7451    ATCGTTTGCT TTACAATGCT ACAACAAACA TCCTTGAACA TGTAAGAAAA
                  TAGCAAACGA AATGTTACGA TGTTGTTTGT AGGAACTTGT ACATTCTTTT
                                  hTRP-2
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          7501    GAGAAAGCGA CCAAGGAACT CCCTTCCCTG CATGTGCTGG TTCTTCATTC
                  CTCTTTCGCT GGTTCCTTGA GGGAAGGGAC GTACACGACC AAGAAGTAAG
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                              hTRP-2
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     7551  CTTTACTGAT GCCATCTTTG ATGAGTGGAT GAAAAGATTT AATCCTCCTG
           GAAATGACTA CGGTAGAAAC TACTCACCTA CTTTTCTAAA TTAGGAGGAC
                              hTRP-2
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     7601  CAGATGCCTG GCCTCAGGAG CTGGCCCCTA TTGGTCACAA TCGGATGTAC
           GTCTACGGAC CGGAGTCCTC GACCGGGGAT AACCAGTGTT AGCCTACATG
                              hTRP-2
           ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
     7651  AACATGGTTC CTTTCTTCCC TCCAGTGACT AATGAAGAAC TCTTTTTAAC
           TTGTACCAAG GAAAGAAGGG AGGTCACTGA TTACTTCTTG AGAAAAATTG
                              hTRP-2
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     7701  CTCAGACCAA CTTGGCTACA GCTATGCCAT CGATCTGCCA GTTTCAGTTG
           GAGTCTGGTT GAACCGATGT CGATACGGTA GCTAGACGGT CAAAGTCAAC
                              hTRP-2
           ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
     7751  AAGAAACTCC AGGTTGGCCC ACAACTCTCT TAGTAGTCAT GGGAACACTG
           TTCTTTGAGG TCCAACCGGG TGTTGAGAGA ATCATCAGTA CCCTTGTGAC
                              hTRP-2
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     7801  GTGGCTTTGG TTGGTCTGTT CGTGCTGTTG GCTTTTCTTC AATATAGAAG
           CACCGAAACC AACCAGACAA GCACGACAAC CGAAAAGAAG TTATATCTTC
                              hTRP-2
           ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
     7851  ACTTCGAAAA GGATATACAC CCCTAATGGA GACACATTTA AGCAGCAAGA
           TGAAGCTTTT CCTATATGTG GGGATTACCT CTGTGTAAAT TCGTCGTTCT
                 hTRP-2
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     7901  GATACACAGA AGAAGCCTAG TTTTTTAATT AAGCATGCTC TAGAATCGAT
           CTATGTGTCT TCTTCGGATC AAAAAATTAA TTCGTACGAG ATCTTAGCTA
                                                  C5 Left Arm
                                                ~~~~~~~~~~~~~~~
     7951  CCCGGGTTTT TATGACTAGT TAATCACGGC CGCTTATAAA GATCTAAAAT
           GGGCCCAAAA ATACTGATCA ATTAGTGCCG GCGAATATTT CTAGATTTTA
                            C5 Left Arm
           ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
     8001  GCATAATTTC TAAATAATGA AAAAAAAGTA CATCATGAGC AACGCGTTAG
           CGTATTAAAG ATTTATTACT TTTTTTTCAT GTAGTACTCG TTGCGCAATC
                            C5 Left Arm
           ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
     8051  TATATTTTAC AATGGAGATT AACGCTCTAT ACCGTTCTAT GTTTATTGAT
           ATATAAAATG TTACCTCTAA TTGCGAGATA TGGCAAGATA CAAATAACTA
                            C5 Left Arm
           ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
     8101  TCAGATGATG TTTTAGAAAA GAAAGTTATT GAATATGAAA ACTTTAATGA
           AGTCTACTAC AAAATCTTTT CTTTCAATAA CTTATACTTT TGAAATTACT
                            C5 Left Arm
           ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
     8151  AGATGAAGAT GACGACGATG ATTATTGTTG TAAATCTGTT TTAGATGAAG
           TCTACTTCTA CTGCTGCTAC TAATAACAAC ATTTAGACAA AATCTACTTC
                            C5 Left Arm
           ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
     8201  AAGATGACGC GCTAAAGTAT ACTATGGTTA CAAAGTATAA GTCTATACTA
           TTCTACTGCG CGATTTCATA TGATACCAAT GTTTCATATT CAGATATGAT
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                              C5 Left Arm
           ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
8251       CTAATGGCGA CTTGTGCAAG AAGGTATAGT ATAGTGAAAA TGTTGTTAGA
           GATTACCGCT GAACACGTTC TTCCATATCA TATCACTTTT ACAACAATCT
                              C5 Left Arm
           ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
8301       TTATGATTAT GAAAAACCAA ATAAATCAGA TCCATATCTA AAGGTATCTC
           AATACTAATA CTTTTTGGTT TATTTAGTCT AGGTATAGAT TTCCATAGAG
                              C5 Left Arm
           ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
8351       CTTTGCACAT AATTTCATCT ATTCCTAGTT TAGAATACTT TTCATTATAT
           GAAACGTGTA TTAAAGTAGA TAAGGATCAA ATCTTATGAA AAGTAATATA
                              C5 Left Arm
           ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
8401       TTGTTTACAG CTGAAGACGA AAAAAATATA TCGATAATAG AAGATTATGT
           AACAAATGTC GACTTCTGCT TTTTTTATAT AGCTATTATC TTCTAATACA
                          C5 Left Arm
           ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
8451       TAACTCTGCT AATAAGATGA AATTGAATGA GTCTGTGACT GCAGCCAAGC
           ATTGAGACGA TTATTCTACT TTAACTTACT CAGACACTGA CGTCGGTTCG
8501       TTGGCACTGG CCGTCGTTTT ACAACGTCGT GACTGGGAAA ACCCTGGCGT
           AACCGTGACC GGCAGCAAAA TGTTGCAGCA CTGACCCTTT TGGGACCGCA
8551       TACCCAACTT AATCGCCTTG CAGCACATCC CCCTTTCGCC AGCTGGCGTA
           ATGGGTTGAA TTAGCGGAAC GTCGTGTAGG GGGAAAGCGG TCGACCGCAT
8601       ATAGCGAAGA GGCCCGCACC GATCGCCCTT CCCAACAGTT GCGCAGCCTG
           TATCGCTTCT CCGGGCGTGG CTAGCGGGAA GGGTTGTCAA CGCGTCGGAC
8651       AATGGCGAAT GGCGCCTGAT GCGGTATTTT CTCCTTACGC ATCTGTGCGG
           TTACCGCTTA CCGCGGACTA CGCCATAAAA GAGGAATGCG TAGACACGCC
8701       TATTTCACAC CGCATATGGT GCACTCTCAG TACAATCTGC TCTGATGCCG
           ATAAAGTGTG GCGTATACCA CGTGAGAGTC ATGTTAGACG AGACTACGGC
8751       CATAGTTAAG CCAGCCCCGA CACCCGCCAA CACCCGCTGA CGCGCCCTGA
           GTATCAATTC GGTCGGGGCT GTGGGCGGTT GTGGGCGACT GCGCGGGACT
8801       CGGGCTTGTC TGCTCCCGGC ATCCGCTTAC AGACAAGCTG TGACCGTCTC
           GCCCGAACAG ACGAGGGCCG TAGGCGAATG TCTGTTCGAC ACTGGCAGAG
8851       CGGGAGCTGC ATGTGTCAGA GGTTTTCACC GTCATCACCG AAACGCGCGA
           GCCCTCGACG TACACAGTCT CCAAAAGTGG CAGTAGTGGC TTTGCGCGCT
8901       GACGAAAGGG CCTCGTGATA CGCCTATTTT TATAGGTTAA TGTCATGATA
           CTGCTTTCCC GGAGCACTAT GCGGATAAAA ATATCCAATT ACAGTACTAT
8951       ATAATGGTTT CTTAGACGTC AGGTGGCACT TTTCGGGGAA ATGTGCGCGG
           TATTACCAAA GAATCTGCAG TCCACCGTGA AAAGCCCCTT TACACGCGCC
9001       AACCCCTATT TGTTTATTTT TCTAAATACA TTCAAATATG TATCCGCTCA
           TTGGGGATAA ACAAATAAAA AGATTTATGT AAGTTTATAC ATAGGCGAGT
9051       TGAGACAATA ACCCTGATAA ATGCTTCAAT AATATTGAAA AAGGAAGAGT
           ACTCTGTTAT TGGGACTATT TACGAAGTTA TTATAACTTT TTCCTTCTCA
                                 Amp(R)
           ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
9101       ATGAGTATTC AACATTTCCG TGTCGCCCTT ATTCCCTTTT TTGCGGCATT
           TACTCATAAG TTGTAAAGGC ACAGCGGGAA TAAGGGAAAA AACGCCGTAA
                                 Amp(R)
           ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
9151       TTGCCTTCCT GTTTTTGCTC ACCCAGAAAC GCTGGTGAAA GTAAAAGATG
           AACGGAAGGA CAAAAACGAG TGGGTCTTTG CGACCACTTT CATTTTCTAC
                                 Amp(R)
           ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
9201       CTGAAGATCA GTTGGGTGCA CGAGTGGGTT ACATCGAACT GGATCTCAAC
           GACTTCTAGT CAACCCACGT GCTCACCCAA TGTAGCTTGA CCTAGAGTTG
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                                Amp(R)
          ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
     9251 AGCGGTAAGA TCCTTGAGAG TTTTCGCCCC GAAGAACGTT TTCCAATGAT
          TCGCCATTCT AGGAACTCTC AAAAGCGGGG CTTCTTGCAA AAGGTTACTA
                                Amp(R)
          ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
     9301 GAGCACTTTT AAAGTTCTGC TATGTGGCGC GGTATTATCC CGTATTGACG
          CTCGTGAAAA TTTCAAGACG ATACACCGCG CCATAATAGG GCATAACTGC
                                Amp(R)
          ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
     9351 CCGGGCAAGA GCAACTCGGT CGCCGCATAC ACTATTCTCA GAATGACTTG
          GGCCCGTTCT CGTTGAGCCA GCGGCGTATG TGATAAGAGT CTTACTGAAC
                                Amp(R)
          ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
     9401 GTTGAGTACT CACCAGTCAC AGAAAAGCAT CTTACGGATG GCATGACAGT
          CAACTCATGA GTGGTCAGTG TCTTTTCGTA GAATGCCTAC CGTACTGTCA
                                Amp(R)
          ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
     9451 AAGAGAATTA TGCAGTGCTG CCATAACCAT GAGTGATAAC ACTGCGGCCA
          TTCTCTTAAT ACGTCACGAC GGTATTGGTA CTCACTATTG TGACGCCGGT
                                Amp(R)
          ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
     9501 ACTTACTTCT GACAACGATC GGAGGACCGA AGGAGCTAAC CGCTTTTTTG
          TGAATGAAGA CTGTTGCTAG CCTCCTGGCT TCCTCGATTG GCGAAAAAAC
                                Amp(R)
          ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
     9551 CACAACATGG GGGATCATGT AACTCGCCTT GATCGTTGGG AACCGGAGCT
          GTGTTGTACC CCCTAGTACA TTGAGCGGAA CTAGCAACCC TTGGCCTCGA
                                Amp(R)
          ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
     9601 GAATGAAGCC ATACCAAACG ACGAGCGTGA CACCACGATG CCTGTAGCAA
          CTTACTTCGG TATGGTTTGC TGCTCGCACT GTGGTGCTAC GGACATCGTT
                                Amp(R)
          ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
     9651 TGGCAACAAC GTTGCGCAAA CTATTAACTG GCGAACTACT TACTCTAGCT
          ACCGTTGTTG CAACGCGTTT GATAATTGAC CGCTTGATGA ATGAGATCGA
                                Amp(R)
          ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
     9701 TCCCGGCAAC AATTAATAGA CTGGATGGAG GCGGATAAAG TTGCAGGACC
          AGGGCCGTTG TTAATTATCT GACCTACCTC CGCCTATTTC AACGTCCTGG
                                Amp(R)
          ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
     9751 ACTTCTGCGC TCGGCCCTTC CGGCTGGCTG GTTTATTGCT GATAAATCTG
          TGAAGACGCG AGCCGGGAAG GCCGACCGAC CAAATAACGA CTATTTAGAC
                                Amp(R)
          ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
     9801 GAGCCGGTGA GCGTGGGTCT CGCGGTATCA TTGCAGCACT GGGGCCAGAT
          CTCGGCCACT CGCACCCAGA GCGCCATAGT AACGTCGTGA CCCCGGTCTA
                                Amp(R)
          ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
     9851 GGTAAGCCCT CCCGTATCGT AGTTATCTAC ACGACGGGGA GTCAGGCAAC
          CCATTCGGGA GGGCATAGCA TCAATAGATG TGCTGCCCCT CAGTCCGTTG
                                Amp(R)
          ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
     9901 TATGGATGAA CGAAATAGAC AGATCGCTGA GATAGGTGCC TCACTGATTA
          ATACCTACTT GCTTTATCTG TCTAGCGACT CTATCCACGG AGTGACTAAT
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Amp(R)
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     9951  AGCATTGGTA ACTGTCAGAC CAAGTTTACT CATATATACT TTAGATTGAT
           TCGTAACCAT TGACAGTCTG GTTCAAATGA GTATATATGA AATCTAACTA
    10001  TTAAAACTTC ATTTTTAATT TAAAAGGATC TAGGTGAAGA TCCTTTTTGA
           AATTTTGAAG TAAAAATTAA ATTTTCCTAG ATCCACTTCT AGGAAAAACT
    10051  TAATCTCATG ACCAAAATCC CTTAACGTGA GTTTTCGTTC CACTGAGCGT
           ATTAGAGTAC TGGTTTTAGG GAATTGCACT CAAAAGCAAG GTGACTCGCA
    10101  CAGACCCCGT AGAAAAGATC AAAGGATCTT CTTGAGATCC TTTTTTTCTG
           GTCTGGGGCA TCTTTTCTAG TTTCCTAGAA GAACTCTAGG AAAAAAAGAC
    10151  CGCGTAATCT GCTGCTTGCA AACAAAAAAA CCACCGCTAC CAGCGGTGGT
           GCGCATTAGA CGACGAACGT TTGTTTTTTT GGTGGCGATG GTCGCCACCA
    10201  TTGTTTGCCG GATCAAGAGC TACCAACTCT TTTTCCGAAG GTAACTGGCT
           AACAAACGGC CTAGTTCTCG ATGGTTGAGA AAAAGGCTTC CATTGACCGA
    10251  TCAGCAGAGC GCAGATACCA AATACTGTCC TTCTAGTGTA GCCGTAGTTA
           AGTCGTCTCG CGTCTATGGT TTATGACAGG AAGATCACAT CGGCATCAAT
    10301  GGCCACCACT TCAAGAACTC TGTAGCACCG CCTACATACC TCGCTCTGCT
           CCGGTGGTGA AGTTCTTGAG ACATCGTGGC GGATGTATGG AGCGAGACGA
    10351  AATCCTGTTA CCAGTGGCTG CTGCCAGTGG CGATAAGTCG TGTCTTACCG
           TTAGGACAAT GGTCACCGAC GACGGTCACC GCTATTCAGC ACAGAATGGC
    10401  GGTTGGACTC AAGACGATAG TTACCGGATA AGGCGCAGCG GTCGGGCTGA
           CCAACCTGAG TTCTGCTATC AATGGCCTAT TCCGCGTCGC CAGCCCGACT
    10451  ACGGGGGGTT CGTGCACACA GCCCAGCTTG GAGCGAACGA CCTACACCGA
           TGCCCCCCAA GCACGTGTGT CGGGTCGAAC CTCGCTTGCT GGATGTGGCT
    10501  ACTGAGATAC CTACAGCGTG AGCTATGAGA AAGCGCCACG CTTCCCGAAG
           TGACTCTATG GATGTCGCAC TCGATACTCT TTCGCGGTGC GAAGGGCTTC
    10551  GGAGAAAGGC GGACAGGTAT CCGGTAAGCG GCAGGGTCGG AACAGGAGAG
           CCTCTTTCCG CCTGTCCATA GGCCATTCGC CGTCCCAGCC TTGTCCTCTC
    10601  CGCACGAGGG AGCTTCCAGG GGGAAACGCC TGGTATCTTT ATAGTCCTGT
           GCGTGCTCCC TCGAAGGTCC CCCTTTGCGG ACCATAGAAA TATCAGGACA
    10651  CGGGTTTCGC CACCTCTGAC TTGAGCGTCG ATTTTTGTGA TGCTCGTCAG
           GCCCAAAGCG GTGGAGACTG AACTCGCAGC TAAAAACACT ACGAGCAGTC
    10701  GGGGGCGGAG CCTATGGAAA AACGCCAGCA ACGCGGCCTT TTTACGGTTC
           CCCCCGCCTC GGATACCTTT TTGCGGTCGT TGCGCCGGAA AAATGCCAAG
    10751  CTGGCCTTTT GCTGGCCTTT TGCTCACATG TTCTTTCCTG CGTTATCCCC
           GACCGGAAAA CGACCGGAAA ACGAGTGTAC AAGAAAGGAC GCAATAGGGG
    10801  TGATTCTGTG GATAACCGTA TTACCGCCTT TGAGTGAGCT GATACCGCTC
           ACTAAGACAC CTATTGGCAT AATGGCGGAA ACTCACTCGA CTATGGCGAG
    10851  GCCGCAGCCG AACGACCGAG CGCAGCGAGT CAGTGAGCGA GGAAGCGGAA
           CGGCGTCGGC TTGCTGGCTC GCGTCGCTCA GTCACTCGCT CCTTCGCCTT
    10901  GAGCGCCCAA TACGCAAACC GCCTCTCCCC GCGCGTTGGC CGATTCATTA
           CTCGCGGGTT ATGCGTTTGG CGGAGAGGGG CGCGCAACCG GCTAAGTAAT
    10951  ATGCAGCTGG CACGACAGGT TTCCCGACTG GAAAGCGGGC AGTGAGCGCA
           TACGTCGACC GTGCTGTCCA AAGGGCTGAC CTTTCGCCCG TCACTCGCGT
    11001  ACGCAATTAA TGTGAGTTAG CTCACTCATT AGGCACCCCA GGCTTTACAC
           TGCGTTAATT ACACTCAATC GAGTGAGTAA TCCGTGGGGT CCGAAATGTG
    11051  TTTATGCTTC CGGCTCGTAT GTTGTGTGGA ATTGTGAGCG GATAACAATT
           AAATACGAAG GCCGAGCATA CAACACACCT TAACACTCGC CTATTGTTAA
    11101  TCACACAGGA AACAGCTATG ACCATGATTA CGAATTGAAT TGCGGCCGCA
           AGTGTGTCCT TTGTCGATAC TGGTACTAAT GCTTAACTTA ACGCCGGCGT
    11151  ATTCTAAG
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FIGURE 4

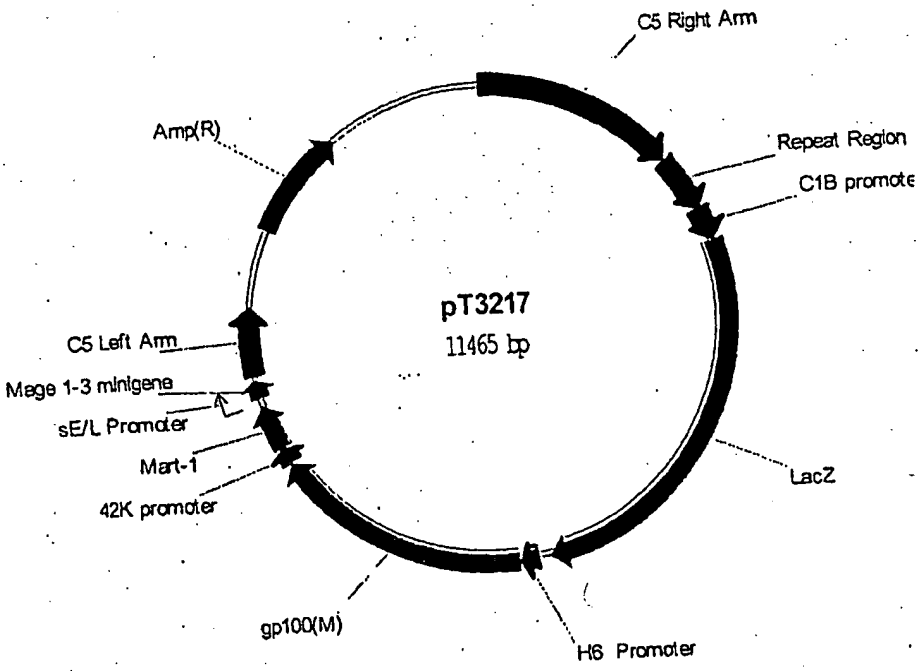

FIGURE 5

DNA Sequence of donor plasmid pT3217

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                          C5 Right Arm
5                ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
       1         TGAATGTTAA ATGTTATACT TTGGATGAAG CTATAAATAT GCATTGGAAA
                 ACTTACAATT TACAATATGA AACCTACTTC GATATTTATA CGTAACCTTT
                          C5 Right Arm
                 ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
10      51       AATAATCCAT TTAAAGAAAG GATTCAAATA CTACAAAACC TAAGCGATAA
                 TTATTAGGTA AATTTCTTTC CTAAGTTTAT GATGTTTTGG ATTCGCTATT
                          C5 Right Arm
                 ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
       101       TATGTTAACT AAGCTTATTC TTAACGACGC TTTAAATATA CACAAATAAA
15               ATACAATTGA TTCGAATAAG AATTGCTGCG AAATTTATAT GTGTTTATTT
                          C5 Right Arm
                 ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
       151       CATAATTTTT GTATAACCTA ACAAATAACT AAAACATAAA AATAATAAAA
                 GTATTAAAAA CATATTGGAT TGTTTATTGA TTTTGTATTT TTATTATTTT
20                        C5 Right Arm
                 ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
       201       GGAAATGTAA TATCGTAATT ATTTTACTCA GGAATGGGGT TAAATATTTA
                 CCTTTACATT ATAGCATTAA TAAAATGAGT CCTTACCCCA ATTTATAAAT
                          C5 Right Arm
25               ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
       251       TATCACGTGT ATATCTATAC TGTTATCGTA TACTCTTTAC AATTACTATT
                 ATAGTGCACA TATAGATATG ACAATAGCAT ATGAGAAATG TTAATGATAA
                          C5 Right Arm
                 ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
30     301       ACGAATATGC AAGAGATAAT AAGATTACGT ATTTAAGAGA ATCTTGTCAT
                 TGCTTATACG TTCTCTATTA TTCTAATGCA TAAATTCTCT TAGAACAGTA
                          C5 Right Arm
                 ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
       351       GATAATTGGG TACGACATAG TGATAAATGC TATTTCGCAT CGTTACATAA
35               CTATTAACCC ATGCTGTATC ACTATTTACG ATAAAGCGTA GCAATGTATT
                          C5 Right Arm
                 ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
       401       AGTCAGTTGG AAAGATGGAT TTGACAGATG TAACTTAATA GGTGCAAAAA
                 TCAGTCAACC TTTCTACCTA AACTGTCTAC ATTGAATTAT CCACGTTTTT
40                        C5 Right Arm
                 ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
       451       TGTTAAATAA CAGCATTCTA TCGGAAGATA GGATACCAGT TATATTATAC
                 ACAATTTATT GTCGTAAGAT AGCCTTCTAT CCTATGGTCA ATATAATATG
                          C5 Right Arm
45               ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
       501       AAAAATCACT GGTTGGATAA AACAGATTCT GCAATATTCG TAAAAGATGA
                 TTTTTAGTGA CCAACCTATT TTGTCTAAGA CGTTATAAGC ATTTTCTACT
                          C5 Right Arm
                 ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
50     551       AGATTACTGC GAATTTGTAA ACTATGACAA TAAAAAGCCA TTTATCTCAA
                 TCTAATGACG CTTAAACATT TGATACTGTT ATTTTTCGGT AAATAGAGTT
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                          C5 Right Arm
                ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
          601   CGACATCGTG TAATTCTTCC ATGTTTTATG TATGTGTTTC AGATATTATG
                GCTGTAGCAC ATTAAGAAGG TACAAAATAC ATACACAAAG TCTATAATAC
                          C5 Right Arm
                ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
          651   AGATTACTAT AAACTTTTTG TATACTTATA TTCCGTAAAC TATATTAATC
                TCTAATGATA TTTGAAAAAC ATATGAATAT AAGGCATTTG ATATAATTAG
                          C5 Right Arm
                ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
          701   ATGAAGAAAA TGAAAAAGTA TAGAAGCTGT TCACGAGCGG TTGTTGAAAA
                TACTTCTTTT ACTTTTTCAT ATCTTCGACA AGTGCTCGCC AACAACTTTT
                          C5 Right Arm
                ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
          751   CAACAAAATT ATACATTCAA GATGGCTTAC ATATACGTCT GTGAGGCTAT
                GTTGTTTTAA TATGTAAGTT CTACCGAATG TATATGCAGA CACTCCGATA
                          C5 Right Arm
                ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
          801   CATGGATAAT GACAATGCAT CTCTAAATAG GTTTTTGGAC AATGGATTCG
                GTACCTATTA CTGTTACGTA GAGATTTATC CAAAAACCTG TTACCTAAGC
                          C5 Right Arm
                ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
          851   ACCCTAACAC GGAATATGGT ACTCTACAAT CTCCTCTTGA AATGGCTGTA
                TGGGATTGTG CCTTATACCA TGAGATGTTA GAGGAGAACT TTACCGACAT
                          C5 Right Arm
                ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
          901   ATGTTCAAGA ATACCGAGGC TATAAAAATC TTGATGAGGT ATGGAGCTAA
                TACAAGTTCT TATGGCTCCG ATATTTTTAG AACTACTCCA TACCTCGATT
                          C5 Right Arm
                ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
          951   ACCTGTAGTT ACTGAATGCA CAACTTCTTG TCTGCATGAT GCGGTGTTGA
                TGGACATCAA TGACTTACGT GTTGAAGAAC AGACGTACTA CGCCACAACT
                          C5 Right Arm
                ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
         1001   GAGACGACTA CAAAATAGTG AAAGATCTGT TGAAGAATAA CTATGTAAAC
                CTCTGCTGAT GTTTTATCAC TTTCTAGACA ACTTCTTATT GATACATTTG
                          C5 Right Arm
                ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
         1051   AATGTTCTTT ACAGCGGAGG CTTTACTCCT TTGTGTTTGG CAGCTTACCT
                TTACAAGAAA TGTCGCCTCC GAAATGAGGA AACACAAACC GTCGAATGGA
                          C5 Right Arm
                ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
         1101   TAACAAAGTT AATTTGGTTA AACTTCTATT GGCTCATTCG GCGGATGTAG
                ATTGTTTCAA TTAAACCAAT TTGAAGATAA CCGAGTAAGC CGCCTACATC
                          C5 Right Arm
                ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
         1151   ATATTTCAAA CACGGATCGG TTAACTCCTC TACATATAGC CGTATCAAAT
                TATAAAGTTT GTGCCTAGCC AATTGAGGAG ATGTATATCG GCATAGTTTA
                          C5 Right Arm
                ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
         1201   AAAAATTTAA CAATGGTTAA ACTTCTATTG AACAAAGGTG CTGATACTGA
                TTTTTAAATT GTTACCAATT TGAAGATAAC TTGTTTCCAC GACTATGACT
                          C5 Right Arm
                ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
         1251   CTTGCTGGAT AACATGGGAT GTACTCCTTT AATGATCGCT GTACAATCTG
                GAACGACCTA TTGTACCCTA CATGAGGAAA TTACTAGCGA CATGTTAGAC
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                          C5 Right Arm
                ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
      1301      GAAATATTGA AATATGTAGC ACACTACTTA AAAAAAATAA AATGTCCAGA
                CTTTATAACT TTATACATCG TGTGATGAAT TTTTTTTATT TTACAGGTCT
                          C5 Right Arm
                ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
      1351      ACTGGGAAAA ATTGATCTTG CCAGCTGTAA TTCATGGTAG AAAAGAAGTG
                TGACCCTTTT TAACTAGAAC GGTCGACATT AAGTACCATC TTTTCTTCAC
                          C5 Right Arm
                ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
      1401      CTCAGGCTAC TTTTCAACAA AGGAGCAGAT GTAAACTACA TCTTTGAAAG
                GAGTCCGATG AAAAGTTGTT TCCTCGTCTA CATTTGATGT AGAAACTTTC
                          C5 Right Arm
                ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
      1451      AAATGGAAAA TCATATACTG TTTTGGAATT GATTAAAGAA AGTTACTCTG
                TTTACCTTTT AGTATATGAC AAAACCTTAA CTAATTTCTT TCAATGAGAC
                          C5 Right Arm
                ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
      1501      AGACACAAAA GAGGTAGCTG AAGTGGTACT CTCAAAGGTA CGTGACTAAT
                TCTGTGTTTT CTCCATCGAC TTCACCATGA GAGTTTCCAT GCACTGATTA
                                              Repeat Region
                                    ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
      1551      TAGCTATAAA AAGGATCGGG TTCTTTATTC TATACTTAAA AAGTGAAAAT
                ATCGATATTT TTCCTAGCCC AAGAAATAAG ATATGAATTT TTCACTTTTA
                          Repeat Region
                ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
      1601      AAATACAAAG GTTCTTGAGG GTTGTGTTAA ATTGAAAGCG AGAAATAATC
                TTTATGTTTC CAAGAACTCC CAACACAATT TAACTTTCGC TCTTTATTAG
                          Repeat Region
                ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
      1651      ATAAATTATT TCATTATCGC GATATCCGTT AAGTTTGTAT CGTAATCTGC
                TATTTAATAA AGTAATAGCG CTATAGGCAA TTCAAACATA GCATTAGACG
                          Repeat Region
                ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
      1701      AGCCCCCACC ATGGATCTGG TGCTAAAAAG ATGCCTTCTT CATTTGGCTG
                TCGGGGGTGG TACCTAGACC ACGATTTTTC TACGGAAGAA GTAAACCGAC
                          Repeat Region
                ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
      1751      TGATAGGTGC TTTGCTGGCT GTGGGGGCTA CAAAAGTACC CAGAAACCAG
                ACTATCCACG AAACGACCGA CACCCCCGAT GTTTTCATGG GTCTTTGGTC
                          Repeat Region
                ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
      1801      GACTGGCTTG GTGTCTCAAG GCAACTCAGA ACCAAAGCCT GGAACAGGCA
                CTGACCGAAC CACAGAGTTC CGTTGAGTCT TGGTTTCGGA CCTTGTCCGT
                          Repeat Region
                ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
      1851      GCTGTATCCA GAGTGGACAG AAGCCCAGAG ACTTGACTGC TGGAGAGGTG
                CGACATAGGT CTCACCTGTC TTCGGGTCTC TGAACTGACG ACCTCTCCAC
                          Repeat Region
                ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
      1901      GTCAAGTGTC CCTCAAGGTC AGTAATGATG GGCCTACACT GATTGGTGCA
                CAGTTCACAG GGAGTTCCAG TCATTACTAC CCGGATGTGA CTAACCACGT
                          Repeat Region
                ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
      1951      AATGCCTCCT TCTCTATTGC CTTGAACTTC CCTGGAAGCC AAAAGGTATT
                TTACGGAGGA AGAGATAACG GAACTTGAAG GGACCTTCGG TTTTCCATAA
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          Repeat Region                    C1B promoter
          ~~~~~~~                  ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
     2001 GCCAGATACT AGTTCTAGAG GATCATTATT TAACGTAAAC TAAATGGAAA
          CGGTCTATGA TCAAGATCTC CTAGTAATAA ATTGCATTTG ATTTACCTTT
                          C1B promoter
          ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
     2051 AGCTATTTAC AGGTACATAC GGTGTTTTTC TGGAATCAAA TGATTCTGAT
          TCGATAAATG TCCATGTATG CCACAAAAAG ACCTTAGTTT ACTAAGACTA
                          C1B promoter
          ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
     2101 TTTGAGGATT TTATCAATAC AATAATGACA GTGCTAACTG GTAAAAAAGA
          AAACTCCTAA AATAGTTATG TTATTACTGT CACGATTGAC CATTTTTTCT
                          C1B promoter
          ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
     2151 AAGCAAACAA TTATCATGGC TAACAATTTT TATTATATTT GTAGTATGCA
          TTCGTTTGTT AATAGTACCG ATTGTTAAAA ATAATATAAA CATCATACGT
                          C1B promoter
          ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
     2201 TAGTGGTCTT TACGTTTCTT TATTTAAAGT TAATGTGTTA AGATTAAATG
          ATCACCAGAA ATGCAAAGAA ATAAATTTCA ATTACACAAT TCTAATTTAC
          C1B promoter                        LacZ
          ~~~~~~~~~~~~~~~          ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
     2251 GAGTAATTGG ATCCCCCATC GATGGGGAAT TCACTGGCCG TCGTTTTACA
          CTCATTAACC TAGGGGGTAG CTACCCCTTA AGTGACCGGC AGCAAAATGT
                          LacZ
          ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
     2301 ACGTCGTGAC TGGGAAAACC CTGGCGTTAC CCAACTTAAT CGCCTTGCAG
          TGCAGCACTG ACCCTTTTGG GACCGCAATG GGTTGAATTA GCGGAACGTC
                           LacZ
          ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
     2351 CACATCCCCC TTTCGCCAGC TGGCGTAATA GCGAAGAGGC CCGCACCGAT
          GTGTAGGGGG AAAGCGGTCG ACCGCATTAT CGCTTCTCCG GGCGTGGCTA
                           LacZ
          ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
     2401 CGCCCTTCCC AACAGTTGCG CAGCCTGAAT GGCGAATGGC GCTTTGCCTG
          GCGGGAAGGG TTGTCAACGC GTCGGACTTA CCGCTTACCG CGAAACGGAC
                           LacZ
          ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
     2451 GTTTCCGGCA CCAGAAGCGG TGCCGGAAAG CTGGCTGGAG TGCGATCTTC
          CAAAGGCCGT GGTCTTCGCC ACGGCCTTTC GACCGACCTC ACGCTAGAAG
                           LacZ
          ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
     2501 CTGAGGCCGA TACTGTCGTC GTCCCCTCAA ACTGGCAGAT GCACGGTTAC
          GACTCCGGCT ATGACAGCAG CAGGGGAGTT TGACCGTCTA CGTGCCAATG
                           LacZ
          ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
     2551 GATGCGCCCA TCTACACCAA CGTGACCTAT CCCATTACGG TCAATCCGCC
          CTACGCGGGT AGATGTGGTT GCACTGGATA GGGTAATGCC AGTTAGGCGG
                           LacZ
          ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
     2601 GTTTGTTCCC ACGGAGAATC CGACGGGTTG TTACTCGCTC ACATTTAATG
          CAAACAAGGG TGCCTCTTAG GCTGCCCAAC AATGAGCGAG TGTAAATTAC
                           LacZ
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     2651 TTGATGAAAG CTGGCTACAG GAAGGCCAGA CGCGAATTAT TTTTGATGGC
          AACTACTTTC GACCGATGTC CTTCCGGTCT GCGCTTAATA AAAACTACCG
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                                LacZ
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     2701       GTTAACTCGG CGTTTCATCT GTGGTGCAAC GGGCGCTGGG TCGGTTACGG
                CAATTGAGCC GCAAAGTAGA CACCACGTTG CCCGCGACCC AGCCAATGCC
                                LacZ
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     2751       CCAGGACAGT CGTTTGCCGT CTGAATTTGA CCTGAGCGCA TTTTTACGCG
                GGTCCTGTCA GCAAACGGCA GACTTAAACT GGACTCGCGT AAAAATGCGC
                                LacZ
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     2801       CCGGAGAAAA CCGCCTCGCG GTGATGGTGC TGCGCTGGAG TGACGGCAGT
                GGCCTCTTTT GGCGGAGCGC CACTACCACG ACGCGACCTC ACTGCCGTCA
                                LacZ
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     2851       TATCTGGAAG ATCAGGATAT GTGGCGGATG AGCGGCATTT TCCGTGACGT
                ATAGACCTTC TAGTCCTATA CACCGCCTAC TCGCCGTAAA AGGCACTGCA
                                LacZ
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     2901       CTCGTTGCTG CATAAACCGA CTACACAAAT CAGCGATTTC CATGTTGCCA
                GAGCAACGAC GTATTTGGCT GATGTGTTTA GTCGCTAAAG GTACAACGGT
                                LacZ
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     2951       CTCGCTTTAA TGATGATTTC AGCCGCGCTG TACTGGAGGC TGAAGTTCAG
                GAGCGAAATT ACTACTAAAG TCGGCGCGAC ATGACCTCCG ACTTCAAGTC
                                LacZ
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     3001       ATGTGCGGCG AGTTGCGTGA CTACCTACGG GTAACAGTTT CTTTATGGCA
                TACACGCCGC TCAACGCACT GATGGATGCC CATTGTCAAA GAAATACCGT
                                LacZ
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     3051       GGGTGAAACG CAGGTCGCCA GCGGCACCGC GCCTTTCGGC GGTGAAATTA
                CCCACTTTGC GTCCAGCGGT CGCCGTGGCG CGGAAAGCCG CCACTTTAAT
                                LacZ
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     3101       TCGATGAGCG TGGTGGTTAT GCCGATCGCG TCACACTACG TCTGAACGTC
                AGCTACTCGC ACCACCAATA CGGCTAGCGC AGTGTGATGC AGACTTGCAG
                                LacZ
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     3151       GAAAACCCGA AACTGTGGAG CGCCGAAATC CCGAATCTCT ATCGTGCGGT
                CTTTTGGGCT TTGACACCTC GCGGCTTTAG GGCTTAGAGA TAGCACGCCA
                                LacZ
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     3201       GGTTGAACTG CACACCGCCG ACGGCACGCT GATTGAAGCA GAAGCCTGCG
                CCAACTTGAC GTGTGGCGGC TGCCGTGCGA CTAACTTCGT CTTCGGACGC
                                LacZ
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     3251       ATGTCGGTTT CCGCGAGGTG CGGATTGAAA ATGGTCTGCT GCTGCTGAAC
                TACAGCCAAA GGCGCTCCAC GCCTAACTTT TACCAGACGA CGACGACTTG
                                LacZ
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     3301       GGCAAGCCGT TGCTGATTCG AGGCGTTAAC CGTCACGAGC ATCATCCTCT
                CCGTTCGGCA ACGACTAAGC TCCGCAATTG GCAGTGCTCG TAGTAGGAGA
                                LacZ
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     3351       GCATGGTCAG GTCATGGATG AGCAGACGAT GGTGCAGGAT ATCCTGCTGA
                CGTACCAGTC CAGTACCTAC TCGTCTGCTA CCACGTCCTA TAGGACGACT
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                                LacZ
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      3401      TGAAGCAGAA CAACTTTAAC GCCGTGCGCT GTTCGCATTA TCCGAACCAT
                ACTTCGTCTT GTTGAAATTG CGGCACGCGA CAAGCGTAAT AGGCTTGGTA
                                LacZ
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      3451      CCGCTGTGGT ACACGCTGTG CGACCGCTAC GGCCTGTATG TGGTGGATGA
                GGCGACACCA TGTGCGACAC GCTGGCGATG CCGGACATAC ACCACCTACT
                                LacZ
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      3501      AGCCAATATT GAAACCCACG GCATGGTGCC AATGAATCGT CTGACCGATG
                TCGGTTATAA CTTTGGGTGC CGTACCACGG TTACTTAGCA GACTGGCTAC
                                LacZ
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      3551      ATCCGCGCTG GCTACCGGCG ATGAGCGAAC GCGTAACGCG AATGGTGCAG
                TAGGCGCGAC CGATGGCCGC TACTCGCTTG CGCATTGCGC TTACCACGTC
                                LacZ
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      3601      CGCGATCGTA ATCACCCGAG TGTGATCATC TGGTCGCTGG GGAATGAATC
                GCGCTAGCAT TAGTGGGCTC ACACTAGTAG ACCAGCGACC CCTTACTTAG
                                LacZ
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      3651      AGGCCACGGC GCTAATCACG ACGCGCTGTA TCGCTGGATC AAATCTGTCG
                TCCGGTGCCG CGATTAGTGC TGCGCGACAT AGCGACCTAG TTTAGACAGC
                                LacZ
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      3701      ATCCTTCCCG CCCGGTGCAG TATGAAGGCG GCGGAGCCGA CACCACGGCC
                TAGGAAGGGC GGGCCACGTC ATACTTCCGC CGCCTCGGCT GTGGTGCCGG
                                LacZ
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      3751      ACCGATATTA TTTGCCCGAT GTACGCGCGC GTGGATGAAG ACCAGCCCTT
                TGGCTATAAT AAACGGGCTA CATGCGCGCG CACCTACTTC TGGTCGGGAA
                                LacZ
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      3801      CCCGGCTGTG CCGAAATGGT CCATCAAAAA ATGGCTTTCG CTACCTGGAG
                GGGCCGACAC GGCTTTACCA GGTAGTTTTT TACCGAAAGC GATGGACCTC
                                LacZ
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      3851      AGACGCGCCC GCTGATCCTT TGCGAATACG CCCACGCGAT GGGTAACAGT
                TCTGCGCGGG CGACTAGGAA ACGCTTATGC GGGTGCGCTA CCCATTGTCA
                                LacZ
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      3901      CTTGGCGGTT TCGCTAAATA CTGGCAGGCG TTTCGTCAGT ATCCCCGTTT
                GAACCGCCAA AGCGATTTAT GACCGTCCGC AAAGCAGTCA TAGGGGCAAA
                                LacZ
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      3951      ACAGGGCGGC TTCGTCTGGG ACTGGGTGGA TCAGTCGCTG ATTAAATATG
                TGTCCCGCCG AAGCAGACCC TGACCCACCT AGTCAGCGAC TAATTTATAC
                                LacZ
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      4001      ATGAAAACGG CAACCCGTGG TCGGCTTACG GCGGTGATTT TGGCGATACG
                TACTTTTGCC GTTGGGCACC AGCCGAATGC CGCCACTAAA ACCGCTATGC
                                LacZ
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      4051      CCGAACGATC GCCAGTTCTG TATGAACGGT CTGGTCTTTG CCGACCGCAC
                GGCTTGCTAG CGGTCAAGAC ATACTTGCCA GACCAGAAAC GGCTGGCGTG
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                                  LacZ
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          4101   GCCGCATCCA GCGCTGACGG AAGCAAAACA CCAGCAGCAG TTTTTCCAGT
                 CGGCGTAGGT CGCGACTGCC TTCGTTTTGT GGTCGTCGTC AAAAAGGTCA
                                  LacZ
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          4151   TCCGTTTATC CGGGCAAACC ATCGAAGTGA CCAGCGAATA CCTGTTCCGT
                 AGGCAAATAG GCCCGTTTGG TAGCTTCACT GGTCGCTTAT GGACAAGGCA
                                  LacZ
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          4201   CATAGCGATA ACGAGCTCCT GCACTGGATG GTGGCGCTGG ATGGTAAGCC
                 GTATCGCTAT TGCTCGAGGA CGTGACCTAC CACCGCGACC TACCATTCGG
                                  LacZ
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          4251   GCTGGCAAGC GGTGAAGTGC CTCTGGATGT CGCTCCACAA GGTAAACAGT
                 CGACCGTTCG CCACTTCACG GAGACCTACA GCGAGGTGTT CCATTTGTCA
                                  LacZ
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          4301   TGATTGAACT GCCTGAACTA CCGCAGCCGG AGAGCGCCGG GCAACTCTGG
                 ACTAACTTGA CGGACTTGAT GGCGTCGGCC TCTCGCGGCC CGTTGAGACC
                                  LacZ
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          4351   CTCACAGTAC GCGTAGTGCA ACCGAACGCG ACCGCATGGT CAGAAGCCGG
                 GAGTGTCATG CGCATCACGT TGGCTTGCGC TGGCGTACCA GTCTTCGGCC
                                  LacZ
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          4401   GCACATCAGC GCCTGGCAGC AGTGGCGTCT GGCGGAAAAC CTCAGTGTGA
                 CGTGTAGTCG CGGACCGTCG TCACCGCAGA CCGCCTTTTG GAGTCACACT
                                  LacZ
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          4451   CGCTCCCCGC CGCGTCCCAC GCCATCCCGC ATCTGACCAC CAGCGAAATG
                 GCGAGGGGCG GCGCAGGGTG CGGTAGGGCG TAGACTGGTG GTCGCTTTAC
                                  LacZ
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          4501   GATTTTTGCA TCGAGCTGGG TAATAAGCGT TGGCAATTTA ACCGCCAGTC
                 CTAAAAACGT AGCTCGACCC ATTATTCGCA ACCGTTAAAT TGGCGGTCAG
                                  LacZ
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          4551   AGGCTTTCTT TCACAGATGT GGATTGGCGA TAAAAAACAA CTGCTGACGC
                 TCCGAAAGAA AGTGTCTACA CCTAACCGCT ATTTTTTGTT GACGACTGCG
                                  LacZ
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          4601   CGCTGCGCGA TCAGTTCACC CGTGCACCGC TGGATAACGA CATTGGCGTA
                 GCGACGCGCT AGTCAAGTGG GCACGTGGCG ACCTATTGCT GTAACCGCAT
                                  LacZ
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          4651   AGTGAAGCGA CCCGCATTGA CCCTAACGCC TGGGTCGAAC GCTGGAAGGC
                 TCACTTCGCT GGGCGTAACT GGGATTGCGG ACCCAGCTTG CGACCTTCCG
                                  LacZ
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          4701   GGCGGGCCAT TACCAGGCCG AAGCAGCGTT GTTGCAGTGC ACGGCAGATA
                 CCGCCCGGTA ATGGTCCGGC TTCGTCGCAA CAACGTCACG TGCCGTCTAT
                                  LacZ
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          4751   CACTTGCTGA TGCGGTGCTG ATTACGACCG CTCACGCGTG GCAGCATCAG
                 GTGAACGACT ACGCCACGAC TAATGCTGGC GAGTGCGCAC CGTCGTAGTC
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                                  LacZ
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4801      GGGAAAACCT TATTTATCAG CCGGAAAACC TACCGGATTG ATGGTAGTGG
          CCCTTTTGGA ATAAATAGTC GGCCTTTTGG ATGGCCTAAC TACCATCACC
                                  LacZ
          ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
4851      TCAAATGGCG ATTACCGTTG ATGTTGAAGT GGCGAGCGAT ACACCGCATC
          AGTTTACCGC TAATGGCAAC TACAACTTCA CCGCTCGCTA TGTGGCGTAG
                                  LacZ
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4901      CGGCGCGGAT TGGCCTGAAC TGCCAGCTGG CGCAGGTAGC AGAGCGGGTA
          GCCGCGCCTA ACCGGACTTG ACGGTCGACC GCGTCCATCG TCTCGCCCAT
                                  LacZ
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4951      AACTGGCTCG GATTAGGGCC GCAAGAAAAC TATCCCGACC GCCTTACTGC
          TTGACCGAGC CTAATCCCGG CGTTCTTTTG ATAGGGCTGG CGGAATGACG
                                  LacZ
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5001      CGCCTGTTTT GACCGCTGGG ATCTGCCATT GTCAGACATG TATACCCCGT
          GCGGACAAAA CTGGCGACCC TAGACGGTAA CAGTCTGTAC ATATGGGGCA
                                  LacZ
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5051      ACGTCTTCCC GAGCGAAAAC GGTCTGCGCT GCGGGACGCG CGAATTGAAT
          TGCAGAAGGG CTCGCTTTTG CCAGACGCGA CGCCCTGCGC GCTTAACTTA
                                  LacZ
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5101      TATGGCCCAC ACCAGTGGCG CGGCGACTTC CAGTTCAACA TCAGCCGGTA
          ATACCGGGTG TGGTCACCGC GCCGCTGAAG GTCAAGTTGT AGTCGGCCAT
                                  LacZ
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5151      CAGTCAACAG CAATTGATGG AAACCAGCCA TTCGCCATCT GCTGCACGCG
          GTCAGTTGTC GTTAACTACC TTTGGTCGGT AAGCGGTAGA CGACGTGCGC
                                  LacZ
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5201      GAAGAGGCAC ATGGCTGAAT ATCGACGGTT TCCATATGGG GATTGGTGGC
          CTTCTCCGTG TACCGACTTA TAGCTGCCAA AGGTATACCC CTAACCACCG
                                  LacZ
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5251      GACGACTCCT GGAGCCCGTC AGTATCGGCG GAATTCCAGC TGAGCGCCGG
          CTGCTGAGGA CCTCGGGCAG TCATAGCCGC CTTAAGGTCG ACTCGCGGCC
                          LacZ
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5301      TCGCTACCAT TACCAGTTGG TCTGGTGTCA AAAATAATAA TAACCGGGCA
          AGCGATGGTA ATGGTCAACC AGACCACAGT TTTTATTATT ATTGGCCCGT
5351      GGGGGGATCC GGAGCTTATC GCAGATCAAT TCGATATCAA GCTTATCGAT
          CCCCCCTAGG CCTCGAATAG CGTCTAGTTA AGCTATAGTT CGAATAGCTA
                                                  H6  Promoter
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5401      ACCGTCGACC TCGAGTCTAG AATCGATCCC GGGTTCTTTA TTCTATACTT
          TGGCAGCTGG AGCTCAGATC TTAGCTAGGG CCCAAGAAAT AAGATATGAA
                               H6  Promoter
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5451      AAAAAGTGAA AATAAATACA AAGGTTCTTG AGGGTTGTGT TAAATTGAAA
          TTTTTCACTT TTATTTATGT TTCCAAGAAC TCCCAACACA ATTTAACTTT
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          H6  Promoter
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    5501  GCGAGAAATA ATCATAAATT ATTTCATTAT CGCGATATCC GTTAAGTTTG
          CGCTCTTTAT TAGTATTTAA TAAAGTAATA GCGCTATAGG CAATTCAAAC
          H6  Promoter                              gp100(M)
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    5551  TATCGTAATC TGCAGCCCCC ACCATGGATC TGGTGCTAAA AAGATGCCTT
          ATAGCATTAG ACGTCGGGGG TGGTACCTAG ACCACGATTT TTCTACGGAA
                                gp100(M)
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    5601  CTTCATTTGG CTGTGATAGG TGCTTTGCTG GCTGTGGGGG CTACAAAAGT
          GAAGTAAACC GACACTATCC ACGAAACGAC CGACACCCCC GATGTTTTCA
                                gp100(M)
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    5651  ACCCAGAAAC CAGGACTGGC TTGGTGTCTC AAGGCAACTC AGAACCAAAG
          TGGGTCTTTG GTCCTGACCG AACCACAGAG TTCCGTTGAG TCTTGGTTTC
                                gp100(M)
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    5701  CCTGGAACAG GCAGCTGTAT CCAGAGTGGA CAGAAGCCCA GAGACTTGAC
          GGACCTTGTC CGTCGACATA GGTCTCACCT GTCTTCGGGT CTCTGAACTG
                                gp100(M)
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    5751  TGCTGGAGAG GTGGTCAAGT GTCCCTCAAG GTCAGTAATG ATGGGCCTAC
          ACGACCTCTC CACCAGTTCA CAGGGAGTTC CAGTCATTAC TACCCGGATG
                                gp100(M)
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    5801  ACTGATTGGT GCAAATGCCT CCTTCTCTAT TGCCTTGAAC TTCCCTGGAA
          TGACTAACCA CGTTTACGGA GGAAGAGATA ACGGAACTTG AAGGGACCTT
                                gp100(M)
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    5851  GCCAAAAGGT ATTGCCAGAT GGGCAGGTTA TCTGGGTCAA CAATACCATC
          CGGTTTTCCA TAACGGTCTA CCCGTCCAAT AGACCCAGTT GTTATGGTAG
                                gp100(M)
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    5901  ATCAATGGGA GCCAGGTGTG GGGAGGACAG CCAGTGTATC CCCAGGAAAC
          TAGTTACCCT CGGTCCACAC CCCTCCTGTC GGTCACATAG GGGTCCTTTG
                                gp100(M)
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    5951  TGACGATGCC TGCATCTTCC CTGATGGTGG ACCTTGCCCA TCTGGCTCTT
          ACTGCTACGG ACGTAGAAGG GACTACCACC TGGAACGGGT AGACCGAGAA
                                gp100(M)
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    6001  GGTCTCAGAA GAGAAGCTTT GTTTATGTCT GGAAGACCTG GGGCCAATAC
          CCAGAGTCTT CTCTTCGAAA CAAATACAGA CCTTCTGGAC CCCGGTTATG
                                gp100(M)
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    6051  TGGCAAGTTC TAGGGGGCCC AGTGTCTGGG CTGAGCATTG GGACAGGCAG
          ACCGTTCAAG ATCCCCCGGG TCACAGACCC GACTCGTAAC CCTGTCCGTC
                                gp100(M)
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    6101  GGCAATGCTG GGCACACACA CGATGGAAGT GACTGTCTAC CATCGCCGGG
          CCGTTACGAC CCGTGTGTGT GCTACCTTCA CTGACAGATG GTAGCGGCCC
                                gp100(M)
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    6151  GATCCCGGAG CTATGTGCCT CTTGCTCATT CCAGCTCAGC CTTCACCATT
          CTAGGGCCTC GATACACGGA GAACGAGTAA GGTCGAGTCG GAAGTGGTAA
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                              gp100(M)
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          6201      ATGGACCAGG TGCCTTTCTC CGTGAGCGTG TCCCAGTTGC GGGCCTTGGA
                    TACCTGGTCC ACGGAAAGAG GCACTCGCAC AGGGTCAACG CCCGGAACCT
                              gp100(M)
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          6251      TGGAGGGAAC AAGCACTTCC TGAGAAATCA GCCTCTGACC TTTGCCCTCC
                    ACCTCCCTTG TTCGTGAAGG ACTCTTTAGT CGGAGACTGG AAACGGGAGG
                              gp100(M)
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          6301      AGCTCCATGA CCCCAGTGGC TATCTGGCTG AAGCTGACCT CTCCTACACC
                    TCGAGGTACT GGGGTCACCG ATAGACCGAC TTCGACTGGA GAGGATGTGG
                              gp100(M)
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          6351      TGGGACTTTG GAGACAGTAG TGGAACCCTG ATCTCTCGGG CACTTGTGGT
                    ACCCTGAAAC CTCTGTCATC ACCTTGGGAC TAGAGAGCCC GTGAACACCA
                              gp100(M)
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          6401      CACTCATACT TACCTGGAGC CTGGCCCAGT CACTGTTCAG GTGGTCCTGC
                    GTGAGTATGA ATGGACCTCG GACCGGGTCA GTGACAAGTC CACCAGGACG
                              gp100(M)
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          6451      AGGCTGCCAT TCCTCTCACC TCCTGTGGCT CCTCCCCAGT TCCAGGCACC
                    TCCGACGGTA AGGAGAGTGG AGGACACCGA GGAGGGGTCA AGGTCCGTGG
                              gp100(M)
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          6501      ACAGATGGGC ACAGGCCAAC TGCAGAGGCC CCTAACACCA CAGCTGGCCA
                    TGTCTACCCG TGTCCGGTTG ACGTCTCCGG GGATTGTGGT GTCGACCGGT
                              gp100(M)
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          6551      AGTGCCTACT ACAGAAGTTG TGGGTACTAC ACCTGGTCAG GCGCCAACTG
                    TCACGGATGA TGTCTTCAAC ACCCATGATG TGGACCAGTC CGCGGTTGAC
                              gp100(M)
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          6601      CAGAGCCCTC TGGAACCACA TCTGTGCAGG TGCCAACCAC TGAAGTCATA
                    GTCTCGGGAG ACCTTGGTGT AGACACGTCC ACGGTTGGTG ACTTCAGTAT
                              gp100(M)
                    ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
          6651      AGCACTGCAC CTGTGCAGAT GCCAACTGCA GAGAGCACAG GTATGACACC
                    TCGTGACGTG GACACGTCTA CGGTTGACGT CTCTCGTGTC CATACTGTGG
                              gp100(M)
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          6701      TGAGAAGGTG CCAGTTTCAG AGGTCATGGG TACCACACTG GCAGAGATGT
                    ACTCTTCCAC GGTCAAAGTC TCCAGTACCC ATGGTGTGAC CGTCTCTACA
                              gp100(M)
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          6751      CAACTCCAGA GGCTACAGGT ATGACACCTG CAGAGGTATC AATTGTGGTG
                    GTTGAGGTCT CCGATGTCCA TACTGTGGAC GTCTCCATAG TTAACACCAC
                              gp100(M)
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          6801      CTTTCTGGAA CCACAGCTGC ACAGGTAACA ACTACAGAGT GGGTGGAGAC
                    GAAAGACCTT GGTGTCGACG TGTCCATTGT TGATGTCTCA CCCACCTCTG
                              gp100(M)
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          6851      CACAGCTAGA GAGCTACCTA TCCCTGAGCC TGAAGGTCCA GATGCCAGCT
                    GTGTCGATCT CTCGATGGAT AGGGACTCGG ACTTCCAGGT CTACGGTCGA
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                                    gp100(M)
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          6901      CAATCATGTC TACGGAAAGT ATTACAGGTT CCCTGGGCCC CCTGCTGGAT
                    GTTAGTACAG ATGCCTTTCA TAATGTCCAA GGGACCCGGG GGACGACCTA
                                    gp100(M)
                    ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
          6951      GGTACAGCCA CCTTAAGGCT GGTGAAGAGA CAAGTCCCCC TGGATTGTGT
                    CCATGTCGGT GGAATTCCGA CCACTTCTCT GTTCAGGGGG ACCTAACACA
                                    gp100(M)
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          7001      TCTGTATCGA TATGGTTCCT TTTCCGTCAC CCTGGACATT GTCCAGGGTA
                    AGACATAGCT ATACCAAGGA AAAGGCAGTG GGACCTGTAA CAGGTCCCAT
                                    gp100(M)
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          7051      TTGAAAGTGC CGAGATCCTG CAGGCTGTGC CGTCCGGTGA GGGGGATGCA
                    AACTTTCACG GCTCTAGGAC GTCCGACACG GCAGGCCACT CCCCCTACGT
                                    gp100(M)
                    ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
          7101      TTTGAGCTGA CTGTGTCCTG CCAAGGCGGG CTGCCCAAGG AAGCCTGCAT
                    AAACTCGACT GACACAGGAC GGTTCCGCCC GACGGGTTCC TTCGGACGTA
                                    gp100(M)
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          7151      GGAGATCTCA TCGCCAGGGT GCCAGCCCCC TGCCCAGCGG CTGTGCCAGC
                    CCTCTAGAGT AGCGGTCCCA CGGTCGGGGG ACGGGTCGCC GACACGGTCG
                                    gp100(M)
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          7201      CTGTGCTACC CAGCCCAGCC TGCCAGCTGG TTCTGCACCA GATACTGAAG
                    GACACGATGG GTCGGGTCGG ACGGTCGACC AAGACGTGGT CTATGACTTC
                                    gp100(M)
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          7251      GGTGGCTCGG GGACATACTG CCTCAATGTG TCTCTGGCTG ATACCAACAG
                    CCACCGAGCC CCTGTATGAC GGAGTTACAC AGAGACCGAC TATGGTTGTC
                                    gp100(M)
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          7301      CCTGGCAGTG GTCAGCACCC AGCTTATCAT GCCTGGTCAA GAAGCAGGCC
                    GGACCGTCAC CAGTCGTGGG TCGAATAGTA CGGACCAGTT CTTCGTCCGG
                                    gp100(M)
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          7351      TTGGGCAGGT TCCGCTGATC GTGGGCATCT TGCTGGTGTT GATGGCTGTG
                    AACCCGTCCA AGGCGACTAG CACCCGTAGA ACGACCACAA CTACCGACAC
                                    gp100(M)
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          7401      GTCCTTGCAT CTCTGATATA TAGGCGCAGA CTTATGAAGC AAGACTTCTC
                    CAGGAACGTA GAGACTATAT ATCCGCGTCT GAATACTTCG TTCTGAAGAG
                                    gp100(M)
                    ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
          7451      CGTACCCCAG TTGCCACATA GCAGCAGTCA CTGGCTGCGT CTACCCCGCA
                    GCATGGGGTC AACGGTGTAT CGTCGTCAGT GACCGACGCA GATGGGGCGT
                                    gp100(M)
                    ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
          7501      TCTTCTGCTC TTGTCCCATT GGTGAGAACA GCCCCCTCCT CAGTGGGCAG
                    AGAAGACGAG AACAGGGTAA CCACTCTTGT CGGGGGAGGA GTCACCCGTC
                    gp100(M)                          42K promoter
                    ~~~~~~~~~                         ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
          7551      CAGGTCTGAT TTTTATTCTA GTTCAAAAAA ATATAAATGA TTCACCATCT
                    GTCCAGACTA AAAATAAGAT CAAGTTTTTT TATATTTACT AAGTGGTAGA
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                        42K promoter
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        7601    GATAGAAAAA AAATTTATTG GGAGAATATG ATAATATTTT GGGATTTCAA
                CTATCTTTTT TTTAAATAAC CCTCTTATAC TATTATAAAA CCCTAAAGTT
5                       42K promoter                          Mart-1
                ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
        7651    AATTGAAAAT ATATAATTAC AATATAAATC TAGACCACCA TGCCAAGAGA
                TTAACTTTTA TATATTAATG TTATATTTAG ATCTGGTGGT ACGGTTCTCT
                                Mart-1
10              ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
        7701    AGATGCTCAC TTCATCTATG GTTACCCCAA GAAGGGGCAC GGCCACTCTT
                TCTACGAGTG AAGTAGATAC CAATGGGGTT CTTCCCCGTG CCGGTGAGAA
                                Mart-1
                ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
15      7751    ACACCACGGC TGAAGAGGCC GCTGGGATCG GCATCCTGAC AGTGATCCTG
                TGTGGTGCCG ACTTCTCCGG CGACCCTAGC CGTAGGACTG TCACTAGGAC
                                Mart-1
                ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
        7801    GGAGTCTTAC TGCTCATCGG CTGTTGGTAT TGTAGAAGAC GAAATGGATA
20              CCTCAGAATG ACGAGTAGCC GACAACCATA ACATCTTCTG CTTTACCTAT
                                Mart-1
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        7851    CAGAGCCTTG ATGGATAAAA GTCTTCATGT TGGCACTCAA TGTGCCTTAA
                GTCTCGGAAC TACCTATTTT CAGAAGTACA ACCGTGAGTT ACACGGAATT
25                              Mart-1
                ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
        7901    CAAGAAGATG CCCACAAGAA GGGTTTGATC ATCGGGACAG CAAAGTGTCT
                GTTCTTCTAC GGGTGTTCTT CCCAAACTAG TAGCCCTGTC GTTTCACAGA
                                Mart-1
30              ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
        7951    CTTCAAGAGA AAAACTGTGA ACCTGTGGTT CCCAATGCTC CACCTGCTTA
                GAAGTTCTCT TTTTGACACT TGGACACCAA GGGTTACGAG GTGGACGAAT
                              Mart-1
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35      8001    TGAGAAACTC TCTGCAGAAC AGTCACCACC ACCTTATTCA CCTTAATCTA
                ACTCTTTGAG AGACGTCTTG TCAGTGGTGG TGGAATAAGT GGAATTAGAT
                                        sE/L Promoter
                                ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
        8051    GAGTCGACCT GCAGGCATGC AAAAATTGAA ATTTTATTTT TTTTTTTTGG
40              CTCAGCTGGA CGTCCGTACG TTTTTAACTT TAAAATAAAA AAAAAAAACC
                sE/L Promoter
                ~~~~~~~~~~~
                                Mage 1-3 minigene
                        ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
45      8101    AATATAAATA ATGGAGTCCT TGCAGCTGGT CTTTGGCATT GACGTGAAGG
                TTATATTTAT TACCTCAGGA ACGTCGACCA GAAACCGTAA CTGCACTTCC
                             Mage 1-3 minigene
                ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
        8151    AAGCAGACCC CACCGGCCAC TCCTATGTCC TTGTCACCTG CCTAGGTCTC
50              TTCGTCTGGG GTGGCCGGTG AGGATACAGG AACAGTGGAC GGATCCAGAG
                             Mage 1-3 minigene
                ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
        8201    TCCTATGATG GCAATAAGCG TAAAGAAGTG GACCCCATCG GCCACTTGTA
                AGGATACTAC CGTTATTCGC ATTTCTTCAC CTGGGGTAGC CGGTGAACAT
55
```

```
      Mage 1-3 minigene                              C5 Left Arm
        ~~~~                                           ~~~~~~~
8251  CTAGTTTTTA TCCCGGGTTT TTATGACTAG TTAATCACGG CCGCTTATAA
      GATCAAAAAT AGGGCCCAAA AATACTGATC AATTAGTGCC GGCGAATATT
                          C5 Left Arm
      ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
8301  AGATCTAAAA TGCATAATTT CTAAATAATG AAAAAAAAGT ACATCATGAG
      TCTAGATTTT ACGTATTAAA GATTTATTAC TTTTTTTTCA TGTAGTACTC
                          C5 Left Arm
      ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
8351  CAACGCGTTA GTATATTTTA CAATGGAGAT TAACGCTCTA TACCGTTCTA
      GTTGCGCAAT CATATAAAAT GTTACCTCTA ATTGCGAGAT ATGGCAAGAT
                          C5 Left Arm
      ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
8401  TGTTTATTGA TTCAGATGAT GTTTTAGAAA AGAAAGTTAT TGAATATGAA
      ACAAATAACT AAGTCTACTA CAAAATCTTT TCTTTCAATA ACTTATACTT
                          C5 Left Arm
      ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
8451  AACTTTAATG AAGATGAAGA TGACGACGAT GATTATTGTT GTAAATCTGT
      TTGAAATTAC TTCTACTTCT ACTGCTGCTA CTAATAACAA CATTTAGACA
                          C5 Left Arm
      ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
8501  TTTAGATGAA GAAGATGACG CGCTAAAGTA TACTATGGTT ACAAAGTATA
      AAATCTACTT CTTCTACTGC GCGATTTCAT ATGATACCAA TGTTTCATAT
                          C5 Left Arm
      ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
8551  AGTCTATACT ACTAATGGCG ACTTGTGCAA GAAGGTATAG TATAGTGAAA
      TCAGATATGA TGATTACCGC TGAACACGTT CTTCCATATC ATATCACTTT
                          C5 Left Arm
      ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
8601  ATGTTGTTAG ATTATGATTA TGAAAAACCA AATAAATCAG ATCCATATCT
      TACAACAATC TAATACTAAT ACTTTTTGGT TTATTTAGTC TAGGTATAGA
                          C5 Left Arm
      ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
8651  AAAGGTATCT CCTTTGCACA TAATTTCATC TATTCCTAGT TTAGAATACT
      TTTCCATAGA GGAAACGTGT ATTAAAGTAG ATAAGGATCA AATCTTATGA
                          C5 Left Arm
      ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
8701  TTTCATTATA TTTGTTTACA GCTGAAGACG AAAAAAATAT ATCGATAATA
      AAAGTAATAT AAACAAATGT CGACTTCTGC TTTTTTTATA TAGCTATTAT
                          C5 Left Arm
      ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
8751  GAAGATTATG TTAACTCTGC TAATAAGATG AAATTGAATG AGTCTGTGAC
      CTTCTAATAC AATTGAGACG ATTATTCTAC TTTAACTTAC TCAGACACTG
      C5 Left Arm
      ~~~~~
8801  TGCAGCCAAG CTTGGCACTG GCCGTCGTTT TACAACGTCG TGACTGGGAA
      ACGTCGGTTC GAACCGTGAC CGGCAGCAAA ATGTTGCAGC ACTGACCCTT
8851  AACCCTGGCG TTACCCAACT TAATCGCCTT GCAGCACATC CCCCTTTCGC
      TTGGGACCGC AATGGGTTGA ATTAGCGGAA CGTCGTGTAG GGGGAAAGCG
8901  CAGCTGGCGT AATAGCGAAG AGGCCCGCAC CGATCGCCCT TCCCAACAGT
      GTCGACCGCA TTATCGCTTC TCCGGGCGTG GCTAGCGGGA AGGGTTGTCA
8951  TGCGCAGCCT GAATGGCGAA TGGCGCCTGA TGCGGTATTT TCTCCTTACG
      ACGCGTCGGA CTTACCGCTT ACCGCGGACT ACGCCATAAA AGAGGAATGC
9001  CATCTGTGCG GTATTTCACA CCGCATATGG TGCACTCTCA GTACAATCTG
      GTAGACACGC CATAAAGTGT GGCGTATACC ACGTGAGAGT CATGTTAGAC
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     9051   CTCTGATGCC GCATAGTTAA GCCAGCCCCG ACACCCGCCA ACACCCGCTG
            GAGACTACGG CGTATCAATT CGGTCGGGGC TGTGGGCGGT TGTGGGCGAC
     9101   ACGCGCCCTG ACGGGCTTGT CTGCTCCCGG CATCCGCTTA CAGACAAGCT
            TGCGCGGGAC TGCCCGAACA GACGAGGGCC GTAGGCGAAT GTCTGTTCGA
     9151   GTGACCGTCT CCGGGAGCTG CATGTGTCAG AGGTTTTCAC CGTCATCACC
            CACTGGCAGA GGCCCTCGAC GTACACAGTC TCCAAAAGTG GCAGTAGTGG
     9201   GAAACGCGCG AGACGAAAGG GCCTCGTGAT ACGCCTATTT TTATAGGTTA
            CTTTGCGCGC TCTGCTTTCC CGGAGCACTA TGCGGATAAA AATATCCAAT
     9251   ATGTCATGAT AATAATGGTT TCTTAGACGT CAGGTGGCAC TTTTCGGGGA
            TACAGTACTA TTATTACCAA AGAATCTGCA GTCCACCGTG AAAAGCCCCT
     9301   AATGTGCGCG GAACCCCTAT TTGTTTATTT TTCTAAATAC ATTCAAATAT
            TTACACGCGC CTTGGGGATA AACAAATAAA AAGATTTATG TAAGTTTATA
     9351   GTATCCGCTC ATGAGACAAT AACCCTGATA AATGCTTCAA TAATATTGAA
            CATAGGCGAG TACTCTGTTA TTGGGACTAT TTACGAAGTT ATTATAACTT
                                      Amp(R)
                    ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
     9401   AAAGGAAGAG TATGAGTATT CAACATTTCC GTGTCGCCCT TATTCCCTTT
            TTTCCTTCTC ATACTCATAA GTTGTAAAGG CACAGCGGGA ATAAGGGAAA
                               Amp(R)
                    ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
     9451   TTTGCGGCAT TTTGCCTTCC TGTTTTTGCT CACCCAGAAA CGCTGGTGAA
            AAACGCCGTA AAACGGAAGG ACAAAAACGA GTGGGTCTTT GCGACCACTT
                               Amp(R)
                    ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
     9501   AGTAAAAGAT GCTGAAGATC AGTTGGGTGC ACGAGTGGGT TACATCGAAC
            TCATTTTCTA CGACTTCTAG TCAACCCACG TGCTCACCCA ATGTAGCTTG
                               Amp(R)
                    ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
     9551   TGGATCTCAA CAGCGGTAAG ATCCTTGAGA GTTTTCGCCC CGAAGAACGT
            ACCTAGAGTT GTCGCCATTC TAGGAACTCT CAAAAGCGGG GCTTCTTGCA
                               Amp(R)
                    ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
     9601   TTTCCAATGA TGAGCACTTT TAAAGTTCTG CTATGTGGCG CGGTATTATC
            AAAGGTTACT ACTCGTGAAA ATTTCAAGAC GATACACCGC GCCATAATAG
                               Amp(R)
                    ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
     9651   CCGTATTGAC GCCGGGCAAG AGCAACTCGG TCGCCGCATA CACTATTCTC
            GGCATAACTG CGGCCCGTTC TCGTTGAGCC AGCGGCGTAT GTGATAAGAG
                               Amp(R)
                    ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
     9701   AGAATGACTT GGTTGAGTAC TCACCAGTCA CAGAAAAGCA TCTTACGGAT
            TCTTACTGAA CCAACTCATG AGTGGTCAGT GTCTTTTCGT AGAATGCCTA
                               Amp(R)
                    ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
     9751   GGCATGACAG TAAGAGAATT ATGCAGTGCT GCCATAACCA TGAGTGATAA
            CCGTACTGTC ATTCTCTTAA TACGTCACGA CGGTATTGGT ACTCACTATT
                               Amp(R)
                    ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
     9801   CACTGCGGCC AACTTACTTC TGACAACGAT CGGAGGACCG AAGGAGCTAA
            GTGACGCCGG TTGAATGAAG ACTGTTGCTA GCCTCCTGGC TTCCTCGATT
                               Amp(R)
                    ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
     9851   CCGCTTTTTT GCACAACATG GGGGATCATG TAACTCGCCT TGATCGTTGG
            GGCGAAAAAA CGTGTTGTAC CCCCTAGTAC ATTGAGCGGA ACTAGCAACC
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                                    Amp(R)
                    ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
          9901      GAACCGGAGC TGAATGAAGC CATACCAAAC GACGAGCGTG ACACCACGAT
                    CTTGGCCTCG ACTTACTTCG GTATGGTTTG CTGCTCGCAC TGTGGTGCTA
                                    Amp(R)
                    ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
          9951      GCCTGTAGCA ATGGCAACAA CGTTGCGCAA ACTATTAACT GGCGAACTAC
                    CGGACATCGT TACCGTTGTT GCAACGCGTT TGATAATTGA CCGCTTGATG
                                    Amp(R)
                    ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
         10001      TTACTCTAGC TTCCCGGCAA CAATTAATAG ACTGGATGGA GGCGGATAAA
                    AATGAGATCG AAGGGCCGTT GTTAATTATC TGACCTACCT CCGCCTATTT
                                    Amp(R)
                    ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
         10051      GTTGCAGGAC CACTTCTGCG CTCGGCCCTT CCGGCTGGCT GGTTTATTGC
                    CAACGTCCTG GTGAAGACGC GAGCCGGGAA GGCCGACCGA CCAAATAACG
                                    Amp(R)
                    ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
         10101      TGATAAATCT GGAGCCGGTG AGCGTGGGTC TCGCGGTATC ATTGCAGCAC
                    ACTATTTAGA CCTCGGCCAC TCGCACCCAG AGCGCCATAG TAACGTCGTG
                                    Amp(R)
                    ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
         10151      TGGGGCCAGA TGGTAAGCCC TCCCGTATCG TAGTTATCTA CACGACGGGG
                    ACCCCGGTCT ACCATTCGGG AGGGCATAGC ATCAATAGAT GTGCTGCCCC
                                    Amp(R)
                    ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
         10201      AGTCAGGCAA CTATGGATGA ACGAAATAGA CAGATCGCTG AGATAGGTGC
                    TCAGTCCGTT GATACCTACT TGCTTTATCT GTCTAGCGAC TCTATCCACG
                           Amp(R)
                    ~~~~~~~~~~~~~~~~~~~~~~~
         10251      CTCACTGATT AAGCATTGGT AACTGTCAGA CCAAGTTTAC TCATATATAC
                    GAGTGACTAA TTCGTAACCA TTGACAGTCT GGTTCAAATG AGTATATATG
         10301      TTTAGATTGA TTTAAAACTT CATTTTTAAT TTAAAAGGAT CTAGGTGAAG
                    AAATCTAACT AAATTTTGAA GTAAAAATTA AATTTTCCTA GATCCACTTC
         10351      ATCCTTTTTG ATAATCTCAT GACCAAAATC CCTTAACGTG AGTTTTCGTT
                    TAGGAAAAAC TATTAGAGTA CTGGTTTTAG GGAATTGCAC TCAAAAGCAA
         10401      CCACTGAGCG TCAGACCCCG TAGAAAAGAT CAAAGGATCT TCTTGAGATC
                    GGTGACTCGC AGTCTGGGGC ATCTTTTCTA GTTTCCTAGA AGAACTCTAG
         10451      CTTTTTTTCT GCGCGTAATC TGCTGCTTGC AAACAAAAAA ACCACCGCTA
                    GAAAAAAAGA CGCGCATTAG ACGACGAACG TTTGTTTTTT TGGTGGCGAT
         10501      CCAGCGGTGG TTTGTTTGCC GGATCAAGAG CTACCAACTC TTTTTCCGAA
                    GGTCGCCACC AAACAAACGG CCTAGTTCTC GATGGTTGAG AAAAAGGCTT
         10551      GGTAACTGGC TTCAGCAGAG CGCAGATACC AAATACTGTC CTTCTAGTGT
                    CCATTGACCG AAGTCGTCTC GCGTCTATGG TTTATGACAG GAAGATCACA
         10601      AGCCGTAGTT AGGCCACCAC TTCAAGAACT CTGTAGCACC GCCTACATAC
                    TCGGCATCAA TCCGGTGGTG AAGTTCTTGA GACATCGTGG CGGATGTATG
         10651      CTCGCTCTGC TAATCCTGTT ACCAGTGGCT GCTGCCAGTG GCGATAAGTC
                    GAGCGAGACG ATTAGGACAA TGGTCACCGA CGACGGTCAC CGCTATTCAG
         10701      GTGTCTTACC GGGTTGGACT CAAGACGATA GTTACCGGAT AAGGCGCAGC
                    CACAGAATGG CCCAACCTGA GTTCTGCTAT CAATGGCCTA TTCCGCGTCG
         10751      GGTCGGGCTG AACGGGGGGT TCGTGCACAC AGCCCAGCTT GGAGCGAACG
                    CCAGCCCGAC TTGCCCCCCA AGCACGTGTG TCGGGTCGAA CCTCGCTTGC
         10801      ACCTACACCG AACTGAGATA CCTACAGCGT GAGCTATGAG AAAGCGCCAC
                    TGGATGTGGC TTGACTCTAT GGATGTCGCA CTCGATACTC TTTCGCGGTG
         10851      GCTTCCCGAA GGGAGAAAGG CGGACAGGTA TCCGGTAAGC GGCAGGGTCG
                    CGAAGGGCTT CCCTCTTTCC GCCTGTCCAT AGGCCATTCG CCGTCCCAGC
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10901   GAACAGGAGA GCGCACGAGG GAGCTTCCAG GGGGAAACGC CTGGTATCTT
        CTTGTCCTCT CGCGTGCTCC CTCGAAGGTC CCCCTTTGCG GACCATAGAA
10951   TATAGTCCTG TCGGGTTTCG CCACCTCTGA CTTGAGCGTC GATTTTTGTG
        ATATCAGGAC AGCCCAAAGC GGTGGAGACT GAACTCGCAG CTAAAAACAC
11001   ATGCTCGTCA GGGGGGCGGA GCCTATGGAA AAACGCCAGC AACGCGGCCT
        TACGAGCAGT CCCCCCGCCT CGGATACCTT TTTGCGGTCG TTGCGCCGGA
11051   TTTTACGGTT CCTGGCCTTT TGCTGGCCTT TTGCTCACAT GTTCTTTCCT
        AAAATGCCAA GGACCGGAAA ACGACCGGAA AACGAGTGTA CAAGAAAGGA
11101   GCGTTATCCC CTGATTCTGT GGATAACCGT ATTACCGCCT TTGAGTGAGC
        CGCAATAGGG GACTAAGACA CCTATTGGCA TAATGGCGGA AACTCACTCG
11151   TGATACCGCT CGCCGCAGCC GAACGACCGA GCGCAGCGAG TCAGTGAGCG
        ACTATGGCGA GCGGCGTCGG CTTGCTGGCT CGCGTCGCTC AGTCACTCGC
11201   AGGAAGCGGA AGAGCGCCCA ATACGCAAAC CGCCTCTCCC CGCGCGTTGG
        TCCTTCGCCT TCTCGCGGGT TATGCGTTTG GCGGAGAGGG GCGCGCAACC
11251   CCGATTCATT AATGCAGCTG GCACGACAGG TTTCCCGACT GGAAAGCGGG
        GGCTAAGTAA TTACGTCGAC CGTGCTGTCC AAAGGGCTGA CCTTTCGCCC
11301   CAGTGAGCGC AACGCAATTA ATGTGAGTTA GCTCACTCAT TAGGCACCCC
        GTCACTCGCG TTGCGTTAAT TACACTCAAT CGAGTGAGTA ATCCGTGGGG
11351   AGGCTTTACA CTTTATGCTT CCGGCTCGTA TGTTGTGTGG AATTGTGAGC
        TCCGAAATGT GAAATACGAA GGCCGAGCAT ACAACACACC TTAACACTCG
11401   GGATAACAAT TTCACACAGG AAACAGCTAT GACCATGATT ACGAATTGAA
        CCTATTGTTA AAGTGTGTCC TTTGTCGATA CTGGTACTAA TGCTTAACTT
11451   TTGCGGCCGC AATTCAACGC CGGCGTTAAG
```

FIGURE 6A

NY-ESO-1

Met Gln Ala Glu Gly Arg Gly Thr Gly Gly Ser Thr Gly Asp Ala Asp
Gly Pro Gly Gly Pro Gly Ile Pro Asp Gly Pro Gly Gly Asn Ala Gly
Gly Pro Gly Glu Ala Gly Ala Thr Gly Gly Arg Gly Pro Arg Gly Ala
Gly Ala Ala Arg Ala Ser Gly Pro Gly Gly Gly Ala Pro Arg Gly Pro
His Gly Gly Ala Ala Ser Gly Leu Asn Gly Cys Cys Arg Cys Gly Ala
Arg Gly Pro Glu Ser Arg Leu Leu Glu Phe Tyr Leu Ala Met Pro Phe
Ala Thr Pro Met Glu Ala Glu Leu Ala Arg Arg Ser Leu Ala Gln Asp
Ala Pro Pro Leu Pro Val Pro Gly Val Leu Leu Lys Glu Phe Thr Val
Ser Gly Asn Ile Leu Thr Ile Arg Leu Thr Ala Ala Asp His Arg Gln
Leu Gln Leu Ser Ile Ser Ser Cys Leu Gln Gln Leu Ser Leu Leu Met
Trp Ile Thr Gln Cys Phe Leu Pro Val Phe Leu Ala Gln Pro Pro Ser
Gly Gln Arg Arg

FIGURE 6C

TRP-2

Met Ser Pro Leu Trp Trp Gly Phe Leu Leu Ser Cys Leu Gly Cys Lys Ile
Leu Pro Gly Ala Gln Gly Gln Phe Pro Arg Val Cys Met Thr Val Asp Ser
Leu Val Asn Lys Glu Cys Cys Pro Arg Leu Gly Ala Glu Ser Ala Asn Val
Cys Gly Ser Gln Gln Gly Arg Gly Gln Cys Thr Glu Val Arg Ala Asp Thr
Arg Pro Trp Ser Gly Pro Tyr Ile Leu Arg Asn Gln Asp Asp Arg Glu Leu
Trp Pro Arg Lys Phe Phe His Arg Thr Cys Lys Cys Thr Gly Asn Phe Ala
Gly Tyr Asn Cys Gly Asp Cys Lys Phe Gly Trp Thr Gly Pro Asn Cys Glu
Arg Lys Lys Pro Pro Val Ile Arg Gln Asn Ile His Ser Leu Ser Pro Gln
Glu Arg Glu Gln Phe Leu Gly Ala Leu Asp Leu Ala Lys Lys Arg Val His
Pro Asp Tyr Val Ile Thr Thr Gln His Trp Leu Gly Leu Leu Gly Pro Asn
Gly Thr Gln Pro Gln Phe Ala Asn Cys Ser Val Tyr Asp Phe Phe Val Trp
Leu His Tyr Tyr Ser Val Arg Asp Thr Leu Leu Gly Pro Gly Arg Pro Tyr
Arg Ala Ile Asp Phe Ser His Gln Gly Pro Ala Phe Val Thr Trp His Arg
Tyr His Leu Leu Cys Leu Glu Arg Asp Leu Gln Arg Leu Ile Gly Asn Glu
Ser Phe Ala Leu Pro Tyr Trp Asn Phe Ala Thr Gly Arg Asn Glu Cys Asp
Val Cys Thr Asp Gln Leu Phe Gly Ala Ala Arg Pro Asp Asp Pro Thr Leu
Ile Ser Arg Asn Ser Arg Phe Ser Ser Trp Glu Thr Val Cys Asp Ser Leu
Asp Asp Tyr Asn His Leu Val Thr Leu Cys Asn Gly Thr Tyr Glu Gly Leu
Leu Arg Arg Asn Gln Met Gly Arg Asn Ser Met Lys Leu Pro Thr Leu Lys
Asp Ile Arg Asp Cys Leu Ser Leu Gln Lys Phe Asp Asn Pro Pro Phe Phe
Gln Asn Ser Thr Phe Ser Phe Arg Asn Ala Leu Glu Gly Phe Asp Lys Ala
Asp Gly Thr Leu Asp Ser Gln Val Met Ser Leu His Asn Leu Val His Ser
Phe Leu Asn Gly Thr Asn Ala Leu Pro His Ser Ala Ala Asn Asp Pro Ile
Phe Val Val Leu His Ser Phe Thr Asp Ala Ile Phe Asp Glu Trp Met Lys
Arg Phe Asn Pro Pro Ala Asp Ala Trp Pro Gln Glu Leu Ala Pro Ile Gly
His Asn Arg Met Tyr Asn Met Val Pro Phe Phe Pro Pro Val Thr Asn Glu
Glu Leu Phe Leu Thr Ser Asp Gln Leu Gly Tyr Ser Tyr Ala Ile Asp Leu
Pro Val Ser Val Glu Glu Thr Pro Gly Trp Pro Thr Thr Leu Leu Val Val
Met Gly Thr Leu Val Ala Leu Val Gly Leu Phe Val Leu Leu Ala Phe Leu
Gln Tyr Arg Arg Leu Arg Lys Gly Tyr Thr Pro Leu Met Glu Thr His Leu
Ser Ser Lys Arg Tyr Thr Glu Glu Ala

FIGURE 6D

gp100 and gp100M

```
1         MDL VLKRCLLHLA VIGALLAVGA TKVPRNQDWL GVSRQLRTKA WNRQLYPEWT
2         *** ********** ********** ********** ********** **********

1 EAQRLDCWRG GQVSLKVSND GPTLIGANAS FSIALNFPGS QKVLPDGQVI WVNNTIINGS
2 ********** ********** ********** ********** ********** **********

1 QVWGGQPVYP QETDDACIFP DGGPCPSGSW SQKRSFVYVW KTWGQYWQFL GGPVSGLSIG
2 ********** ********** ********** ********** *********V* **********

1 TGRAMLGTHT MEVTVYHRRG SRSYVPLAHS SSAFTITDQV PFSVSVSQLR ALDGGNKHFL
2 ********** ********** ********** ******M*** ********** **********

1 RNQPLTFALQ LHDPSGYLAE ADLSYTWDFG DSSGTLISRA LVVTHTYLEP GPVTAQVVLQ
2 ********** ********** ********** ********** ********** ****V*****

1 AAIPLTSCGS SPVPGTTDGH RPTAEAPNTT AGQVPTTEVV GTTPGQAPTA EPSGTTSVQV
2 ********** ********** ********** ********** ********** **********

1 PTTEVISTAP VQMPTAESTG MTPEKVPVSE VMGTTLAEMS TPEATGMTPA EVSIVVLSGT
2 ********** ********** ********** ********** ********** **********

1 TAAQVTTTEW VETTARELPI PEPEGPDASS IMSTESITGS LGPLLDGTAT LRLVKRQVPL
2 ********** ********** ********** ********** ********** **********

1 DCVLYRYGSF SVTLDIVQGI ESAEILQAVP SGEGDAFELT VSCQGGLPKE ACMEISSPGC
2 ********** ********** ********** ********** ********** **********

1 QPPAQRLCQP VLPSPACQLV LHQILKGGSG TYCLNVSLAD TNSLAVVSTQ LIMPGQEAGL
2 ********** ********** ********** ********** ********** **********

1 GQVPLIVGIL LVLMAVVLAS LIYRRRLMKQ DFSVPQLPHS SSHWLRLPRI FCSCPIGENS
2 ********** ********** ********** ********** ********** **********

1 PLLSGQQV2 ********
```

Key
*=identical amino acid residue
1=gp100
2=gp100M

FIGURE 6E

MART-1

Met Pro Arg Glu Asp Ala His Phe Ile Tyr Gly Tyr Pro
Lys Lys Gly His Gly His Ser Tyr Thr Thr Ala Glu Glu
Ala Ala Gly Ile Gly Ile Leu Thr Val Ile Leu Gly Val
Leu Leu Leu Ile Gly Cys Trp Tyr Cys Arg Arg Arg Asn
Gly Tyr Arg Ala Leu Met Asp Lys Ser Leu His Val Gly
Thr Gln Cys Ala Leu Thr Arg Arg Cys Pro Gln Glu Gly
Phe Asp His Arg Asp Ser Lys Val Ser Leu Gln Glu Lys
Asn Cys Glu Pro Val Val Pro Asn Ala Pro Pro Ala Tyr
Glu Lys Leu Ser Ala Glu Gln Ser Pro Pro Pro Tyr Ser
Pro

FIGURE 6F

MAGE-1

Met Ser Asp Asn Lys Lys Pro Asp Lys Ala His Ser Gly Ser Gly Gly
Asp Gly Asp Gly Asn Arg Cys Asn Leu Leu His Arg Tyr Ser Leu Glu
Glu Ile Leu Pro Tyr Leu Gly Trp Leu Val Phe Ala Val Val Thr Thr
Ser Phe Leu Ala Leu Gln Met Phe Ile Asp Ala Leu Tyr Glu Glu Gln
Tyr Glu Arg Asp Val Ala Trp Ile Ala Arg Gln Ser Lys Arg Met Ser
Ser Val Asp Glu Asp Glu Asp Asp Glu Asp Asp Glu Asp Asp Tyr Tyr
Asp Asp Glu Asp Asp Asp Asp Asp Ala Phe Tyr Asp Asp Glu Asp Asp
Glu Glu Glu Glu Leu Glu Asn Leu Met Asp Asp Glu Ser Glu Asp Glu
Ala Glu Glu Glu Met Ser Val Glu Met Gly Ala Gly Ala Glu Glu Met
Gly Ala Gly Ala Asn Cys Ala Cys Val Pro Gly His His Leu Arg Lys
Asn Glu Val Lys Cys Arg Met Ile Tyr Phe Phe His Asp Pro Asn Phe
Leu Val Ser Ile Pro Val Asn Pro Lys Glu Gln Met Glu Cys Arg Cys
Glu Asn Ala Asp Glu Glu Val Ala Met Glu Glu Glu Glu Glu Glu Glu
Glu Glu Glu Glu Glu Glu Glu Glu Met Gly Asn Pro Asp Gly Phe Ser Pro

FIGURE 6G

MAGE-3

mpleqrsqhc kpeeglearg ealglvgaqa pateeqeaas ssstlvevtl gevpaaespd
ppqspqgass lpttmnyplw sqsyedssnq eeegpstfpd lesefqaals rkvaelvhfl
llkyrarepv tkaemlgsvv gnwqyffpvi fskassslql vfgielmevd pighlyifat
clglsydgll gdnqimpkag lliivlaiia regdcapeek iweelsvlev fegredsilg
dpkkllтqhf vqenyleyrq vpgsdpacye flwgpralve tsyvkvlhhm vkisggphis
ypplhewvlr egee

FIGURE 6H
B7.1

mghtrrqgts pskcpylnff qllvlaglsh fcsgvihvtk evkevatlsc ghnvsveela
qtriywqkek kmvltmmsgd mniwpeyknr tifditnnls ivilalrpsd egtyecvvlk
yekdafkreh laevtlsvka dfptpsisdf eiptsnirri icstsggfpe phlswlenge
elnainttvs qdpetelyav sskldfnmtt nhsfmcliky ghlrvnqtfn wnttkqehfp
dnllpswait lisvngifvi ccltycfapr crerrrnerl rresvrpv

FIGURE 6I
LFA-3

mvagsdagra lgvlsvvcll hcfgfiscfs qqiygvvygn vtfhvpsnvp lkevlwkkqk
dkvaelense frafssfknr vyldtvsgsl tiynltssde deyemespni tdtmkfflyv
leslpsptlt caltngsiev qcmipehyns hrglimyswd cpmeqckrns tsiyfkmend
lpqkiqctls nplfnttssi ilttcipssg hsrhryalip iplavittci vlymngilkc
drkpdrtnsn

FIGURE 6J
ICAM-1*

mapssprpal pallvllgal fpgpgnaqts vspskvilpr ggsvlvtcst scdqpkllgi
etplpkkell lpgnnrkvye lsnvqedsqp mcysncpdgq staktfltvy wtpervelap
lpswqpvgkn ltlrcqvegg apranltvvl lrgekelkre pavgepaevt ttvlvrrdhh
ganfscrtel dlrpqglelf entsapyqlq tfvlpatppq lvsprvlevd tqgtvvcsld
glfpvseaqv hlalgdqrln ptvtygndsf sakasvsvta edegtqrltc avilgnqsqe
tlqtvtiysf papnviltkp evsegtevtv kceahprakv tlngvpaqpl gpraqlllka
tpedngrsfs csatlevagq lihknqtrel rvlygprlde rdcpgnwtwp ensqqtpmcq
awgnplpelk clkdgtfplp igesvtvtrd legtylcrar stqgevtrev tvnvlsprye
iviitvvaaa vimgtaglst ylynrqrkik kyrlqqaqkg tpmkpntqat pp

*mature sequence begins at residue 28 (q)